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(71) Applicants (for all designated States except US): CALGENE LLC [US/US]; 1920 Fifth Street, Davis, CA 95616 (US).		Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>			
(54) Title: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS IN PLANTS					
(57) Abstract					
<p>The present invention relates to compositions and methods for preparing polyunsaturated long chain fatty acids in plants, plant parts and plant cells, such as leaves, roots, fruits and seeds. Nucleic acid sequences and constructs encoding fatty acid desaturases, including $\Delta 5$-desaturases, $\Delta 6$-desaturases and $\Delta 12$-desaturases, are used to generate transgenic plants, plant parts and cells which contain and express one or more transgenes encoding one or more desaturases. Expression of the desaturases with different substrate specificities in the plant system permit the large scale production of polyunsaturated long chain fatty acids such as docosahexaenoic acid, eicosapentaenoic acid, α-linolenic acid, gamma-linolenic acid, arachidonic acid and the like for modification of the fatty acid profile of plants, plant parts and tissues. Manipulation of the fatty acid profiles allows for the production of commercial quantities of novel plant oils and products.</p>					
<pre> graph TD PA[Palmitic Acid (C16)] --> SA[Stearic Acid (C18)] SA --> OA[Oleic Acid] OA --> LA[Linoleic Acid] LA --> ALA[α-Linolenic Acid] ALA --> DHA[DH-γ-Linolenic Acid (Elcoicenoic)] DHA --> AA[Arachidonic Acid] AA --> PG1[Prostaglandin G1] AA --> PG2[Prostaglandin E2, F2] AA --> PG3[Prostaglandin G2] PA --> P1[Palmitoleic (C16Δ)] SA --> P2[γ-Linolenic Acid] P2 --> DGLA[Δ-5, 12, 15-Stearidonic Acid] DGLA --> PG1 DGLA --> PG2 DGLA --> PG3 OA --> P3[Δ-5, 12, 14-Eicosadienoic Acid] P3 --> PG1 P3 --> PG2 P3 --> PG3 DHA --> P4[Δ-5, 12, 14-Eicosatrienoic Acid] P4 --> PG1 P4 --> PG2 P4 --> PG3 </pre>					

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**METHODS AND COMPOSITIONS FOR SYNTHESIS OF
LONG CHAIN POLYUNSATURATED FATTY ACIDS IN PLANTS**

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of USSN 08/834,655, filed April 11, 1997, and a continuation in part of USSN 08/833,610, filed April 11, 1997, USSN 08/834,033 filed April 11, 1997 and USSN 08/956,985 filed October 24, 1997 which disclosures are incorporated herein by reference.

INTRODUCTION

Field of the Invention

10 This invention relates to modulating levels of enzymes and/or enzyme components capable of altering the production of long chain polyunsaturated fatty acids (PUFAS) in a host plant. The invention is exemplified by the production of PUFAS in plants.

Background

15 Two main families of polyunsaturated fatty acids (PUFAs) are the $\omega 3$ fatty acids, exemplified by arachidonic acid, and the $\omega 6$ fatty acids, exemplified by eicosapentaenoic acid. PUFAs are important components of the plasma membrane of the cell, where they may be found in such forms as phospholipids. PUFAs also serve as precursors to other molecules of importance in human beings and animals, including the prostacyclins, leukotrienes and prostaglandins. PUFAs are necessary for proper development, particularly in the developing infant brain, and for tissue formation and repair.

20 Four major long chain PUFAs of importance include docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA), which are primarily found in different types of fish oil, gamma-linolenic acid (GLA), which is found in the seeds of a number of plants, including evening primrose (*Oenothera biennis*), borage (*Borago officinalis*) and black currants (*Ribes nigrum*), and stearidonic acid (SDA), which is found in marine oils and plant seeds. Both GLA and another important long chain PUFA, arachidonic acid (ARA), are found in

filamentous fungi. ARA can be purified from animal tissues including liver and adrenal gland.

- For DHA, a number of sources exist for commercial production including a variety of marine organisms, oils obtained from cold water marine fish, and egg yolk fractions. For ARA, microorganisms including the genera *Mortierella*, *Entomophthora*, *Phytium* and *Porphyridium* can be used for commercial production. Commercial sources of SDA include the genera *Trichodesma* and *Echium*. Commercial sources of GLA include evening primrose, black currants and borage. However, there are several disadvantages associated with commercial production of PUFAs from natural sources. Natural sources of PUFAs, such as animals and plants, tend to have highly heterogeneous oil compositions. The oils obtained from these sources therefore can require extensive purification to separate out one or more desired PUFAs or to produce an oil which is enriched in one or more PUFA. Natural sources also are subject to uncontrollable fluctuations in availability. Fish stocks may undergo natural variation or may be depleted by overfishing. Fish oils have unpleasant tastes and odors, which may be impossible to economically separate from the desired product, and can render such products unacceptable as food supplements. Animal oils, and particularly fish oils, can accumulate environmental pollutants. Weather and disease can cause fluctuation in yields from both fish and plant sources. Cropland available for production of alternate oil-producing crops is subject to competition from the steady expansion of human populations and the associated increased need for food production on the remaining arable land. Crops which do produce PUFAs, such as borage, have not been adapted to commercial growth and may not perform well in monoculture. Growth of such crops is thus not economically competitive where more profitable and better established crops can be grown. Large scale fermentation of organisms such as *Mortierella* is also expensive. Natural animal tissues contain low amounts of ARA and are difficult to process.
- Microorganisms such as *Porphyridium* and *Mortierella* are difficult to cultivate on a commercial scale.

Dietary supplements and pharmaceutical formulations containing PUFAs can retain the disadvantages of the PUFA source. Supplements such as fish oil capsules can contain low levels of the particular desired component and thus require large dosages. High dosages result in ingestion of high levels of

5 undesired components, including contaminants. Care must be taken in providing fatty acid supplements, as overaddition may result in suppression of endogenous biosynthetic pathways and lead to competition with other necessary fatty acids in various lipid fractions *in vivo*, leading to undesirable results. For example, Eskimos having a diet high in $\omega 3$ fatty acids have an increased

10 tendency to bleed (U.S. Pat. No. 4,874,603). Unpleasant tastes and odors of the supplements can make such regimens undesirable, and may inhibit compliance by the patient.

A number of enzymes are involved in PUFA biosynthesis. Linoleic acid (LA, 18:2 $\Delta 9, 12$) is produced from oleic acid (18:1 $\Delta 9$) by a $\Delta 12$ -desaturase.

15 GLA (18:3 $\Delta 6, 9, 12$) is produced from linoleic acid (LA, 18:2 $\Delta 9, 12$) by a $\Delta 6$ -desaturase. ARA (20:4 $\Delta 5, 8, 11, 14$) production from DGLA (20:3 $\Delta 8, 11, 14$) is catalyzed by a $\Delta 5$ -desaturase. However, animals cannot desaturate beyond the $\Delta 9$ position and therefore cannot convert oleic acid (18:1 $\Delta 9$) into linoleic acid (18:2 $\Delta 9, 12$). Likewise, α -linolenic acid (ALA, 18:3 $\Delta 9, 12, 15$) cannot

20 be synthesized by mammals. Other eukaryotes, including fungi and plants, have enzymes which desaturate at positions $\Delta 21$ and $\Delta 15$. The major poly-unsaturated fatty acids of animals therefore are either derived from diet and/or from desaturation and elongation of linoleic acid (18:2 $\Delta 9, 12$) or α -linolenic acid (18:3 $\Delta 9, 12, 15$).

25 Poly-unsaturated fatty acids are considered to be useful for nutritional, pharmaceutical, industrial, and other purposes. An expansive supply of poly-unsaturated fatty acids from natural sources and from chemical synthesis are not sufficient for commercial needs. Therefore it is of interest to obtain genetic material involved in PUFA biosynthesis from species that naturally produce

30 these fatty acids and to express the isolated material alone or in combination in

a heterologous system which can be manipulated to allow production of commercial quantities of PUFAS.

The present invention is further directed to formulas, dietary supplements or dietary supplements in the form of a liquid or a solid containing 5 the long chain fatty acids of the invention. These formulas and supplements may be administered to a human or an animal.

The formulas and supplements of the invention may further comprise at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed 10 whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

The formulas of the present invention may further include at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of 15 calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

The present invention is further directed to a method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to the patient a dietary substitute of the 20 invention in an amount sufficient to effect treatment of the patient.

The present invention is further directed to cosmetic and pharmaceutical compositions of the material of the invention.

The present invention is further directed to transgenic oils in pharmaceutically acceptable carriers. The present invention is further directed 25 to nutritional supplements, cosmetic agents and infant formulae containing transgenic oils.

The present invention is further directed to a method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of: growing a microbe having cells which contain a transgene which encodes a

transgene expression product which desaturates a fatty acid molecule at carbon 5,5 or 12 from the carboxyl end of said fatty acid molecule, wherein the transgene is operably associated with an expression control sequence, under conditions whereby the transgene is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in the cells is altered.

5 The present invention is further directed toward pharmaceutical compositions comprising at least one nutrient selected from the group consisting of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

10 **Relevant Literature**

Production of gamma-linolenic acid by a $\Delta 6$ -desaturase is described in USPN 5,552,306 and USPN 5,614,393. Production of 8, 11-eicosadienoic acid using *Mortierella alpina* is disclosed in USPN 5,376,541. Production of docosahexaenoic acid by dinoflagellates is described in USPN 5,407,957.

15 Cloning of a $\Delta 6$ -desaturase from borage is described in PCT publication WO 96/21022. Cloning of $\Delta 9$ -desaturases is described in the published patent applications PCT WO 91/13972, EP 0 550 162 A1, EP 0 561 569 A2, EP 0 644 263 A2, and EP 0 736 598 A1, and in USPN 5,057,419. Cloning of $\Delta 12$ -desaturases from various organisms is described in PCT publication WO

20 94/11516 and USPN 5,443,974. Cloning of $\Delta 15$ -desaturases from various organisms is described in PCT publication WO 93/11245. A $\Delta 6$ palmitoyl-acyl carrier protein desaturase from *Thumbergia alata* and its expression in *E. coli* is described in USPN 5,614,400. Expression of a soybean stearyl-ACP desaturase in transgenic soybean embryos using a 35S promoter is disclosed in USPN

25 5,443,974.

SUMMARY OF THE INVENTION

Novel compositions and methods are provided for preparation of poly-unsaturated long chain fatty acids and desaturases in plants and plant cells. The methods involve growing a host plant cell of interest transformed with an expression cassette functional in a host plant cell, the expression cassette

comprising a transcriptional and translational initiation regulatory region, joined in reading frame 5' to a DNA sequence encoding a desaturase polypeptide capable of modulating the production of PUFAs. Expression of the desaturase polypeptide provides for an alteration in the PUFA profile of host plant cells as 5 a result of altered concentrations of enzymes involved in PUFA biosynthesis. Of particular interest is the selective control of PUFA production in plant tissues and/or plant parts such as leaves, roots, fruits and seeds. The invention finds use for example in the large scale production of DHA, EPA, ARA, and GLA and for modification of the fatty acid profile of edible plant tissues and/or plant 10 parts.

The present invention further includes a purified nucleotide sequence or polypeptide sequence that is substantially related or homologous to the nucleotide and peptide sequences presented in SEQ ID NO:1 - SEQ ID NO:52. The present invention is further directed to methods of using the sequences 15 presented in SEQ ID NO:1 to SEQ ID NO:40 as probes to identify related sequences, as components of expression systems and as components of systems useful for producing transgenic oil.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows possible pathways for the synthesis of arachidonic acid 20 (20:4 Δ5, 8, 11, 14) and stearidonic acid (18:4 Δ6, 9, 12, 15) from palmitic acid (C₁₆) from a variety of organisms, including algae, *Mortierella* and humans. These PUFAs can serve as precursors to other molecules important for humans and other animals, including prostacyclins, leukotrienes, and prostaglandins, some of which are shown.

25 Figure 2 shows possible pathways for production of PUFAs in addition to ARA, including EPA and DHA, again compiled from a variety of organisms.

Figure 3A-E shows the DNA sequence (SEQ ID NO:1) of the *Mortierella alpina* Δ6 desaturase and the deduced amino acid sequence (SEQ ID NO:2).

Figure 4 shows an alignment of the *Mortierella alpina* Δ6 desaturase amino acid sequence with other Δ6 desaturases and related sequences (SEQ ID NOS:7, 8, 9, 10, 11, 12 and 13).

Figure 5A-D shows the DNA sequence of the *Mortierella alpina* Δ12 desaturase (SEQ ID NO:3) and the deduced amino acid sequence (SEQ ID NO:4)

Figure 6 shows the deduced amino acid sequence (SEQ ID NO:14) of the PCR fragment (see Example 1).

Figure 7A-D shows the DNA sequence of the *Mortierella alpina* Δ5 desaturase (SEQ ID NO:5).

Figure 8 shows alignments of the protein sequence of the Δ5 desaturase (SEQ ID NO:6) with Δ6 desaturases and related sequences (SEQ ID NOS:15, 16, 17, 18).

Figure 9 shows alignments of the protein sequence of the Ma 29 and contig 253538a.

Figure 10 shows alignments of the protein sequence of Ma 524 and contig 253538a.

BRIEF DESCRIPTION OF THE SEQUENCE LISTINGS

SEQ ID NO:1 shows the DNA sequence of the *Mortierella alpina* Δ6 desaturase.

SEQ ID NO:2 shows the amino acid sequence of the *Mortierella alpina* Δ6 desaturase.

SEQ ID NO:3 shows the DNA sequence of the *Mortierella alpina* Δ12 desaturase.

SEQ ID NO:4 shows the amino acid sequence of the *Mortierella alpina* Δ12 desaturase.

SEQ ID NO:5 shows the DNA sequence of the *Mortierella alpina* Δ5 desaturase.

SEQ ID NO:6 shows the amino acid sequence *Mortierella alpina* Δ5 desaturase.

5 SEQ ID NO:7 - SEQ ID NO:13 show amino acid sequences that relate to *Mortierella alpina* Δ6 desaturase.

SEQ ID NO:14 shows an amino acid sequence of a PCR fragment of Example 1.

10 SEQ ID NO:15 - SEQ ID NO:18 show amino acid sequences that relate to *Mortierella alpina* Δ5 and Δ6 desaturases.

SEQ ID NO:19 - SEQ ID NO:30 show PCR primer sequences.

SEQ ID NO:31 - SEQ ID NO:37 show human nucleotide sequences.

SEQ ID NO:38 - SEQ ID NO:44 show human peptide sequences.

15 SEQ ID NO:45 - SEQ ID NO:46 show the nucleotide and amino acid sequence of a *Dictyostelium discoideum* desaturase.

SEQ ID NO:47 - SEQ ID NO:50 show the nucleotide and deduced amino acid sequence of a *Schizochytrium* cDNA clone.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

In order to ensure a complete understanding of the invention, the 20 following definitions are provided:

Δ5-Desaturase: Δ5 desaturase is an enzyme which introduces a double bond between carbons 5 and 6 from the carboxyl end of a fatty acid molecule.

Δ6-Desaturase: Δ6-desaturase is an enzyme which introduces a double bond between carbons 6 and 7 from the carboxyl end of a fatty acid molecule.

25 **Δ9-Desaturase:** Δ9-desaturase is an enzyme which introduces a double bond between carbons 9 and 10 from the carboxyl end of a fatty acid molecule.

Δ12-Desaturase: Δ12-desaturase is an enzyme which introduces a double bond between carbons 12 and 13 from the carboxyl end of a fatty acid molecule.

Fatty Acids: Fatty acids are a class of compounds containing a long

- 5 hydrocarbon chain and a terminal carboxylate group. Fatty acids include the following:

Fatty Acid		
12:0	lauric acid	
16:0	palmitic acid	
16:1	palmitoleic acid	
18:0	stearic acid	
18:1	oleic acid	Δ9-18:1
18:2 Δ5,9	taxoleic acid	Δ5,9-18:2
18:2 Δ6,9	6,9-octadecadienoic acid	Δ6,9-18:2
18:2	linoleic acid	Δ9,12-18:2 (LA)
18:3 Δ6,9,12	gamma-linolenic acid	Δ6,9,12-18:3 (GLA)
18:3 Δ5,9,12	pinolenic acid	Δ5,9,12-18:3
18:3	alpha-linolenic acid	Δ9,12,15-18:3 (ALA)
18:4	stearidonic acid	Δ6,9,12,15-18:4 (SDA)
20:0	Arachidic acid	
20:1	Eicoscenic Acid	
22:0	behehic acid	
22:1	erucic acid	
22:2	Docasadienoic acid	
20:4 ω6	arachidonic acid	Δ5,8,11,14-20:4 (ARA)
20:3 ω6	ω6-eicosatrienoic dihomo-gamma linolenic	Δ8,11,14-20:3 (DGLA)
20:5 ω3	Eicosapentanoic (Timnodonic acid)	Δ5,8,11,14,17-20:5 (EPA)
20:3 ω3	ω3-eicosatrienoic	Δ11,16,17-20:3
20:4 ω3	ω3-eicosatetraenoic	Δ8,11,14,17-20:4
22:5 ω3	Docosapentaenoic	Δ7,10,13,16,19-22:5 (ω3DPA)
22:6 ω3	Docosahexaenoic (cervonic acid)	Δ4,7,10,13,16,19-22:6 (DHA)
24:0	Lignoceric acid	

Taking into account these definitions, the present invention is directed to novel DNA sequences, DNA constructs, methods and compositions are provided which permit modification of the poly-unsaturated long chain fatty acid content of plant cells. Plant cells are transformed with an expression cassette

5 comprising a DNA encoding a polypeptide capable of increasing the amount of one or more PUFA in a plant cell. Desirably, integration constructs may be prepared which provide for integration of the expression cassette into the genome of a host cell. Host cells are manipulated to express a sense or antisense DNA encoding a polypeptide(s) that has desaturase activity. By

10 "desaturase" is intended a polypeptide which can desaturate one or more fatty acids to produce a mono- or poly-unsaturated fatty acid or precursor thereof of interest. By "polypeptide" is meant any chain of amino acids, regardless of length or post-translational modification, for example, glycosylation or phosphorylation. The substrate(s) for the expressed enzyme may be produced

15 by the host cell or may be exogenously supplied.

To achieve expression in a host cell, the transformed DNA is operably associated with transcriptional and translational initiation and termination regulatory regions that are functional in the host cell. Constructs comprising the gene to be expressed can provide for integration into the genome of the host cell

20 or can autonomously replicate in the host cell. For production of linoleic acid (LA), the expression cassettes generally used include a cassette which provides for $\Delta 12$ desaturase activity, particularly in a host cell which produces or can take up oleic acid. For production of ALA, the expression cassettes generally used include a cassette which provides for $\Delta 15$ or $\omega 3$ desaturase activity,

25 particularly in a host cell which produces or can take up LA. For production of GLA or SDA, the expression cassettes generally used include a cassette which provides for $\Delta 6$ desaturase activity, particularly in a host cell which produces or can take up LA or ALA, respectively. Production of $\omega 6$ -type unsaturated fatty acids, such as LA or GLA, is favored in a plant capable of producing ALA by

30 inhibiting the activity of a $\Delta 15$ or $\omega 3$ type desaturase; this is accomplished by providing an expression cassette for an antisense $\Delta 15$ or $\omega 3$ transcript, or by

disrupting a Δ 15 or ω 3 desaturase gene. Similarly, production of LA or ALA is favored in a plant having Δ 6 desaturase activity by providing an expression cassette for an antisense Δ 6 transcript, or by disrupting a Δ 6 desaturase gene. Production of oleic acid likewise is favored in a plant having Δ 12 desaturase

5 activity by providing an expression cassette for an antisense Δ 12 transcript, or by disrupting a Δ 12 desaturase gene. For production of ARA, the expression cassette generally used provides for Δ 5 desaturase activity, particularly in a host cell which produces or can take up DGLA. Production of ω 6-type unsaturated fatty acids, such as ARA, is favored in a plant capable of producing ALA by

10 inhibiting the activity of a Δ 15 or ω 3 type desaturase; this is accomplished by providing an expression cassette for an antisense Δ 15 or ω 3 transcript, or by disrupting a Δ 15 or ω 3 desaturase gene.

TRANSGENIC PLANT PRODUCTION OF FATTY ACIDS

Transgenic plant production of PUFAs offers several advantages over

15 purification from natural sources such as fish or plants. Production of fatty acids from recombinant plants provides the ability to alter the naturally occurring plant fatty acid profile by providing new synthetic pathways in the host or by suppressing undesired pathways, thereby increasing levels of desired PUFAs, or conjugated forms thereof, and decreasing levels of undesired

20 PUFAs. Production of fatty acids in transgenic plants also offers the advantage that expression of desaturase genes in particular tissues and/or plant parts means that greatly increased levels of desired PUFAs in those tissues and/or parts can be achieved, making recovery from those tissues more economical. For example, the desired PUFAs can be expressed in seed; methods of isolating

25 seed oils are well established. In addition to providing a source for purification of desired PUFAs, seed oil components can be manipulated through expression of desaturase genes, either alone or in combination with other genes such as elongases, to provide seed oils having a particular PUFA profile in concentrated form. The concentrated seed oils then can be added to animal milks and/or

30 synthetic or semi-synthetic milks to serve as infant formulas where human

nursing is impossible or undesired, or in cases of malnourishment or disease in both adults and infants.

For production of PUFAs, depending upon the host cell, the availability of substrate, and the desired end product(s), several polypeptides, particularly 5 desaturases, are of interest including those polypeptides which catalyze the conversion of stearic acid to oleic acid, LA to GLA, of ALA to SDA, of oleic acid to LA, or of LA to ALA, which includes enzymes which desaturate at the $\Delta 6$, $\Delta 9$, $\Delta 12$, $\Delta 15$ or $\omega 3$ positions. Considerations for choosing a specific polypeptide having desaturase activity include the pH optimum of the 10 polypeptide, whether the polypeptide is a rate limiting enzyme or a component thereof, whether the desaturase used is essential for synthesis of a desired poly-unsaturated fatty acid, and/or co-factors required by the polypeptide. The expressed polypeptide preferably has parameters compatible with the biochemical environment of its location in the host cell. For example, the 15 polypeptide may have to compete for substrate with other enzymes in the host cell. Analyses of the K_m and specific activity of the polypeptide in question therefore are considered in determining the suitability of a given polypeptide for modifying PUFA production in a given host cell. The polypeptide used in a particular situation therefore is one which can function under the conditions 20 present in the intended host cell but otherwise can be any polypeptide having desaturase activity which has the desired characteristic of being capable of modifying the relative production of a desired PUFA. A scheme for the synthesis of arachidonic acid (20:4 $\Delta 5, 8, 11, 14$) from palmitic acid (C_{16}) is shown in Figure 1. A key enzyme in this pathway is a $\Delta 5$ -desaturase which 25 converts DH- γ -linolenic acid (DGLA, eicosatrienoic acid) to ARA. Conversion of α -linolenic acid (ALA) to stearidonic acid by a $\Delta 6$ -desaturase is also shown. Production of PUFAs in addition to ARA, including EPA and DHA is shown in Figure 2. A key enzyme in the synthesis of arachidonic acid (20:4 $\Delta 5, 8, 11, 14$) from stearic acid (C_{18}) is a $\Delta 6$ -desaturase which converts the linoleic acid 30 into γ -linolenic acid. Conversion of α -linolenic acid (ALA) to stearidonic acid by a $\Delta 6$ -desaturase also is shown. For production of ARA, the DNA sequence

used encodes a polypeptide having $\Delta 5$ desaturase activity. In particular instances, this can be coupled with an expression cassette which provides for production of a polypeptide having $\Delta 6$ desaturase activity and, optionally, a transcription cassette providing for production of antisense sequences to a $\Delta 15$ transcription product. The choice of combination of cassettes used depends in part on the PUFA profile of the host cell. Where the host cell $\Delta 5$ -desaturase activity is limiting, overexpression of $\Delta 5$ desaturase alone generally will be sufficient to provide for enhanced ARA production.

SOURCES OF POLYPEPTIDES HAVING DESATURASE ACTIVITY

As sources of polypeptides having desaturase activity and oligonucleotides encoding such polypeptides are organisms which produce a desired poly-unsaturated fatty acid. As an example, microorganisms having an ability to produce ARA can be used as a source of $\Delta 5$ -desaturase genes; 15 microorganisms which GLA or SDA can be used as a source of $\Delta 6$ -desaturase and/or $\Delta 12$ -desaturase genes. Such microorganisms include, for example, those belonging to the genera *Mortierella*, *Conidiobolus*, *Pythium*, *Phytophthora*, *Penicillium*, *Porphyridium*, *Coidosporium*, *Mucor*, *Fusarium*, *Aspergillus*, *Rhodotorula*, and *Entomophthora*. Within the genus *Porphyridium*, of 20 particular interest is *Porphyridium cruentum*. Within the genus *Mortierella*, of particular interest are *Mortierella elongata*, *Mortierella exigua*, *Mortierella hygrophila*, *Mortierella ramanniana*, var. *angulispora*, and *Mortierella alpina*. Within the genus *Mucor*, of particular interest are *Mucor circinelloides* and *Mucor javanicus*.

25 DNAs encoding desired desaturases can be identified in a variety of ways. As an example, a source of the desired desaturase, for example genomic or cDNA libraries from *Mortierella*, is screened with detectable enzymatically- or chemically-synthesized probes, which can be made from DNA, RNA, or non-naturally occurring nucleotides, or mixtures thereof. Probes may be 30 enzymatically synthesized from DNAs of known desaturases for normal or

reduced-stringency hybridization methods. Oligonucleotide probes also can be used to screen sources and can be based on sequences of known desaturases, including sequences conserved among known desaturases, or on peptide sequences obtained from the desired purified protein. Oligonucleotide probes 5 based on amino acid sequences can be degenerate to encompass the degeneracy of the genetic code, or can be biased in favor of the preferred codons of the source organism. Oligonucleotides also can be used as primers for PCR from reverse transcribed mRNA from a known or suspected source; the PCR product can be the full length cDNA or can be used to generate a probe to obtain the 10 desired full length cDNA. Alternatively, a desired protein can be entirely sequenced and total synthesis of a DNA encoding that polypeptide performed.

Once the desired genomic or cDNA has been isolated, it can be sequenced by known methods. It is recognized in the art that such methods are subject to errors, such that multiple sequencing of the same region is routine and 15 is still expected to lead to measurable rates of mistakes in the resulting deduced sequence, particularly in regions having repeated domains, extensive secondary structure, or unusual base compositions, such as regions with high GC base content. When discrepancies arise, resequencing can be done and can employ special methods. Special methods can include altering sequencing conditions 20 by using: different temperatures; different enzymes; proteins which alter the ability of oligonucleotides to form higher order structures; altered nucleotides such as ITP or methylated dGTP; different gel compositions, for example adding formamide; different primers or primers located at different distances from the problem region; or different templates such as single stranded DNAs. 25 Sequencing of mRNA can also be employed.

For the most part, some or all of the coding sequence for the polypeptide having desaturase activity is from a natural source. In some situations, however, it is desirable to modify all or a portion of the codons, for example, to enhance expression, by employing host preferred codons. Host preferred 30 codons can be determined from the codons of highest frequency in the proteins expressed in the largest amount in a particular host species of interest. Thus, the

- coding sequence for a polypeptide having desaturase activity can be synthesized in whole or in part. All or portions of the DNA also can be synthesized to remove any destabilizing sequences or regions of secondary structure which would be present in the transcribed mRNA. All or portions of
- 5 the DNA also can be synthesized to alter the base composition to one more preferable in the desired host cell. Methods for synthesizing sequences and bringing sequences together are well established in the literature. *In vitro* mutagenesis and selection, site-directed mutagenesis, or other means can be employed to obtain mutations of naturally occurring desaturase genes to
- 10 produce a polypeptide having desaturase activity *in vivo* with more desirable physical and kinetic parameters for function in the host cell, such as a longer half-life or a higher rate of production of a desired polyunsaturated fatty acid.

Desirable cDNAs have less than 60% A+T composition, preferably less than 50% A+T composition. On a localized scale of a sliding window of 20 base pairs, it is preferable that there are no localized regions of the cDNA with greater than 75% A+T composition; with a window of 60 base pairs, it is preferable that there are no localized regions of the cDNA with greater than 60%, more preferably no localized regions with greater than 55% A+T composition.

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Mortierella alpina Desaturases

Of particular interest are the *Mortierella alpina* $\Delta 5$ -desaturase, $\Delta 6$ -desaturase and $\Delta 12$ -desaturase. The $\Delta 5$ -desaturase has 446 amino acids; the amino acid sequence is shown in Figure 7. The gene encoding the *Mortierella alpina* $\Delta 5$ -desaturase can be expressed in transgenic microorganisms to effect

25 greater synthesis of ARA from DGLA. Other DNAs which are substantially identical in sequence to the *Mortierella alpina* $\Delta 5$ -desaturase DNA, or which encode polypeptides which are substantially identical in sequence to the *Mortierella alpina* $\Delta 5$ -desaturase polypeptide, also can be used. The *Mortierella alpina* $\Delta 6$ -desaturase, has 457 amino acids and a predicted

30 molecular weight of 51.8 kD; the amino acid sequence is shown in Figure 3.

The gene encoding the *Mortierella alpina* Δ6-desaturase can be expressed in transgenic plants or animals to effect greater synthesis of GLA from linoleic acid or of stearidonic acid (SDA) from ALA. Other DNAs which are substantially identical in sequence to the *Mortierella alpina* Δ6-desaturase

- 5 DNA, or which encode polypeptides which are substantially identical in sequence to the *Mortierella alpina* Δ6-desaturase polypeptide, also can be used.

The *Mortierella alpina* Δ12-desaturase has the amino acid sequence shown in Figure 5. The gene encoding the *Mortierella alpina* Δ12-desaturase can be expressed in transgenic plants to effect greater synthesis of LA from 10 oleic acid. Other DNAs which are substantially identical to the *Mortierella alpina* Δ12-desaturase DNA, or which encode polypeptides which are substantially identical to the *Mortierella alpina* Δ12-desaturase polypeptide, also can be used.

By substantially identical in sequence is intended an amino acid 15 sequence or nucleic acid sequence exhibiting in order of increasing preference at least 60%, 80%, 90% or 95% homology to the *Mortierella alpina* Δ5-desaturase amino acid sequence or nucleic acid sequence encoding the amino acid sequence. For polypeptides, the length of comparison sequences generally is at least 16 amino acids, preferably at least 20 amino acids, or most preferably 20 35 amino acids. For nucleic acids, the length of comparison sequences generally is at least 50 nucleotides, preferably at least 60 nucleotides, and more preferably at least 75 nucleotides, and most preferably, 110 nucleotides. Homology typically is measured using sequence analysis software, for example, the Sequence Analysis software package of the Genetics Computer Group, 25 University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wisconsin 53705, MEGAlign (DNAStar, Inc., 1228 S. Park St., Madison, Wisconsin 53715), and MacVector (Oxford Molecular Group, 2105 S. Bascom Avenue, Suite 200, Campbell, California 95008). Such software matches similar sequences by assigning degrees of homology to various 30 substitutions, deletions, and other modifications. Conservative substitutions typically include substitutions within the following groups: glycine and alanine;

valine, isoleucine and leucine; aspartic acid, glutamic acid, asparagine, and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine. Substitutions may also be made on the basis of conserved hydrophobicity or hydrophilicity (Kyte and Doolittle, *J. Mol. Biol.* 157: 105-132, 1982), or on the basis of the ability to assume similar polypeptide secondary structure (Chou and Fasman, *Adv. Enzymol.* 47: 45-148, 1978).

Other Desaturases

Encompassed by the present invention are related desaturases from the same or other organisms. Such related desaturases include variants of the disclosed $\Delta 5$ -, $\Delta 6$ - and $\Delta 12$ -desaturases that occur naturally within the same or different species of *Mortierella*, as well as homologues of the disclosed $\Delta 5$ -desaturase from other species and evolutionarily related protein having desaturase activity. Also included are desaturases which, although not substantially identical to the *Mortierella alpina* $\Delta 5$ -desaturase, desaturate a fatty acid molecule at carbon 5, 6 or 12, respectively, from the carboxyl end of a fatty acid molecule. Related desaturases can be identified by their ability to function substantially the same as the disclosed desaturases; that is, are still able to effectively convert DGLA to ARA, LA to GLA, ALA to SDA or oleic acid to LA. Related desaturases also can be identified by screening sequence databases for sequences homologous to the disclosed desaturase, by hybridization of a probe based on the disclosed desaturase to a library constructed from the source organism, or by RT-PCR using mRNA from the source organism and primers based on the disclosed desaturase. Such desaturases includes those from humans, *Dictyostelium discoideum* and *Phaeodactylum tricornutum*.

The regions of a desaturase polypeptide important for desaturase activity can be determined through routine mutagenesis, expression of the resulting mutant polypeptides and determination of their activities. Mutants may include deletions, insertions and point mutations, or combinations thereof. A typical functional analysis begins with deletion mutagenesis to determine the N- and C-terminal limits of the protein necessary for function, and then internal deletions,

insertions or point mutants are made to further determine regions necessary for function. Other techniques such as cassette mutagenesis or total synthesis also can be used. Deletion mutagenesis is accomplished, for example, by using exonucleases to sequentially remove the 5' or 3' coding regions. Kits are

5 available for such techniques. After deletion, the coding region is completed by ligating oligonucleotides containing start or stop codons to the deleted coding region after 5' or 3' deletion, respectively. Alternatively, oligonucleotides encoding start or stop codons are inserted into the coding region by a variety of methods including site-directed mutagenesis, mutagenic PCR or by ligation

10 onto DNA digested at existing restriction sites. Internal deletions can similarly be made through a variety of methods including the use of existing restriction sites in the DNA, by use of mutagenic primers via site directed mutagenesis or mutagenic PCR. Insertions are made through methods such as linker-scanning mutagenesis, site-directed mutagenesis or mutagenic PCR. Point mutations are

15 made through techniques such as site-directed mutagenesis or mutagenic PCR.

Chemical mutagenesis can also be used for identifying regions of a desaturase polypeptide important for activity. A mutated construct is expressed, and the ability of the resulting altered protein to function as a desaturase is assayed. Such structure-function analysis can determine which regions may be

20 deleted, which regions tolerate insertions, and which point mutations allow the mutant protein to function in substantially the same way as the native desaturase. All such mutant proteins and nucleotide sequences encoding them are within the scope of the present invention.

EXPRESSION OF DESATURASE GENES

Once the DNA encoding a desaturase polypeptide has been obtained, it is placed in a vector capable of replication in a host cell, or is propagated *in vitro* by means of techniques such as PCR or long PCR. Replicating vectors can include plasmids, phage, viruses, cosmids and the like. Desirable vectors include those useful for mutagenesis of the gene of interest or for expression of

25 the gene of interest in host cells. The technique of long PCR has made *in vitro* propagation of large constructs possible, so that modifications to the gene of

interest, such as mutagenesis or addition of expression signals, and propagation of the resulting constructs can occur entirely *in vitro* without the use of a replicating vector or a host cell.

For expression of a desaturase polypeptide, functional transcriptional and translational initiation and termination regions are operably linked to the DNA encoding the desaturase polypeptide. Transcriptional and translational initiation and termination regions are derived from a variety of nonexclusive sources, including the DNA to be expressed, genes known or suspected to be capable of expression in the desired system, expression vectors, chemical synthesis, or from an endogenous locus in a host cell. Expression in a plant tissue and/or plant part presents certain efficiencies, particularly where the tissue or part is one which is easily harvested, such as seed, leaves, fruits, flowers, roots, etc. Expression can be targeted to that location within the plant by using specific regulatory sequences, such as those of USPN 5,463,174, USPN 4,943,674, USPN 5,106,739, USPN 5,175,095, USPN 5,420,034, USPN 5,188,958, and USPN 5,589,379. Alternatively, the expressed protein can be an enzyme which produces a product which may be incorporated, either directly or upon further modifications, into a fluid fraction from the host plant. In the present case, expression of desaturase genes, or antisense desaturase transcripts, can alter the levels of specific PUFAs, or derivatives thereof, found in plant parts and/or plant tissues. The Δ5-desaturase polypeptide coding region is expressed either by itself or with other genes, in order to produce tissues and/or plant parts containing higher proportions of desired PUFAs or in which the PUFA composition more closely resembles that of human breast milk (Prieto *et al.*, PCT publication WO 95/24494). The termination region can be derived from the 3' region of the gene from which the initiation region was obtained or from a different gene. A large number of termination regions are known to and have been found to be satisfactory in a variety of hosts from the same and different genera and species. The termination region usually is selected more as a matter of convenience rather than because of any particular property.

The choice of a host cell is influenced in part by the desired PUFA profile of the transgenic cell, and the native profile of the host cell. As an example, for production of linoleic acid from oleic acid, the DNA sequence used encodes a polypeptide having $\Delta 12$ desaturase activity, and for production of GLA from linoleic acid, the DNA sequence used encodes a polypeptide having $\Delta 6$ desaturase activity. Use of a host cell which expresses $\Delta 12$ desaturase activity and lacks or is depleted in $\Delta 15$ desaturase activity, can be used with an expression cassette which provides for overexpression of $\Delta 6$ desaturase alone generally is sufficient to provide for enhanced GLA production in the transgenic cell. Where the host cell expresses $\Delta 9$ desaturase activity, expression of both a $\Delta 12$ - and a $\Delta 6$ -desaturase can provide for enhanced GLA production. In particular instances where expression of $\Delta 6$ desaturase activity is coupled with expression of $\Delta 12$ desaturase activity, it is desirable that the host cell naturally have, or be mutated to have, low $\Delta 15$ desaturase activity.

Alternatively, a host cell for $\Delta 6$ desaturase expression may have, or be mutated to have, high $\Delta 12$ desaturase activity.

Expression in a host cell can be accomplished in a transient or stable fashion. Transient expression can occur from introduced constructs which contain expression signals functional in the host cell, but which constructs do not replicate and rarely integrate in the host cell, or where the host cell is not proliferating. Transient expression also can be accomplished by inducing the activity of a regulatable promoter operably linked to the gene of interest, although such inducible systems frequently exhibit a low basal level of expression. Stable expression can be achieved by introduction of a construct that can integrate into the host genome or that autonomously replicates in the host cell. Stable expression of the gene of interest can be selected for through the use of a selectable marker located on or transfected with the expression construct, followed by selection for cells expressing the marker. When stable expression results from integration, integration of constructs can occur randomly within the host genome or can be targeted through the use of constructs containing regions of homology with the host genome sufficient to

target recombination with the host locus. Where constructs are targeted to an endogenous locus, all or some of the transcriptional and translational regulatory regions can be provided by the endogenous locus.

When increased expression of the desaturase polypeptide in the source
5 plant is desired, several methods can be employed. Additional genes encoding
the desaturase polypeptide can be introduced into the host organism.
Expression from the native desaturase locus also can be increased through
homologous recombination, for example by inserting a stronger promoter into
the host genome to cause increased expression, by removing destabilizing
10 sequences from either the mRNA or the encoded protein by deleting that
information from the host genome, or by adding stabilizing sequences to the
mRNA (*see* USPN 4,910,141 and USPN 5,500,365.)

When it is desirable to express more than one different gene, appropriate
regulatory regions and expression methods, introduced genes can be propagated
15 in the host cell through use of replicating vectors or by integration into the host
genome. Where two or more genes are expressed from separate replicating
vectors, it is desirable that each vector has a different means of replication.
Each introduced construct, whether integrated or not, should have a different
means of selection and should lack homology to the other constructs to maintain
20 stable expression and prevent reassortment of elements among constructs.
Judicious choices of regulatory regions, selection means and method of
propagation of the introduced construct can be experimentally determined so
that all introduced genes are expressed at the necessary levels to provide for
synthesis of the desired products.

25 Constructs comprising the gene of interest may be introduced into a host
cell by standard techniques. These techniques include transfection, infection,
bolistic impact, electroporation, microinjection, scraping, or any other method
which introduces the gene of interest into the host cell (*see* USPN 4,743,548,
USPN 4,795,855, USPN 5,068,193, USPN 5,188,958, USPN 5,463,174, USPN
30 5,565,346 and USPN 5,565,347). For convenience, a host cell which has been
manipulated by any method to take up a DNA sequence or construct will be

referred to as "transformed" or "recombinant" herein. The subject host will have at least have one copy of the expression construct and may have two or more, depending upon whether the gene is integrated into the genome, amplified, or is present on an extrachromosomal element having multiple copy numbers.

- 5 The transformed host cell can be identified by selection for a marker contained on the introduced construct. Alternatively, a separate marker construct may be introduced with the desired construct, as many transformation techniques introduce many DNA molecules into host cells. Typically,
- 10 transformed hosts are selected for their ability to grow on selective media. Selective media may incorporate an antibiotic or lack a factor necessary for growth of the untransformed host, such as a nutrient or growth factor. An introduced marker gene therefor may confer antibiotic resistance, or encode an essential growth factor or enzyme, and permit growth on selective media when
- 15 expressed in the transformed host cell. Desirably, resistance to kanamycin and the amino glycoside G418 are of interest (*see* USPN 5,034,322). Selection of a transformed host can also occur when the expressed marker protein can be detected, either directly or indirectly. The marker protein may be expressed alone or as a fusion to another protein. The marker protein can be detected by
- 20 its enzymatic activity; for example β galactosidase can convert the substrate X-gal to a colored product, and luciferase can convert luciferin to a light-emitting product. The marker protein can be detected by its light-producing or modifying characteristics; for example, the green fluorescent protein of *Aequorea victoria* fluoresces when illuminated with blue light. Antibodies can
- 25 be used to detect the marker protein or a molecular tag on, for example, a protein of interest. Cells expressing the marker protein or tag can be selected, for example, visually, or by techniques such as FACS or panning using antibodies.
- 30 The PUFAs produced using the subject methods and compositions may be found in the host plant tissue and/or plant part as free fatty acids or in conjugated forms such as acylglycerols, phospholipids, sulfolipids or

glycolipids, and may be extracted from the host cell through a variety of means well-known in the art. Such means may include extraction with organic solvents, sonication, supercritical fluid extraction using for example carbon dioxide, and physical means such as presses, or combinations thereof.

5. particular interest is extraction with hexane or methanol and chloroform. Where desirable, the aqueous layer can be acidified to protonate negatively charged moieties and thereby increase partitioning of desired products into the organic layer. After extraction, the organic solvents can be removed by evaporation under a stream of nitrogen. When isolated in conjugated forms, the products are
- 10 enzymatically or chemically cleaved to release the free fatty acid or a less complex conjugate of interest, and are then subjected to further manipulations to produce a desired end product. Desirably, conjugated forms of fatty acids are cleaved with potassium hydroxide.

PURIFICATION OF FATTY ACIDS

- 15 If further purification is necessary, standard methods can be employed. Such methods include extraction, treatment with urea, fractional crystallization, HPLC, fractional distillation, silica gel chromatography, high speed centrifugation or distillation, or combinations of these techniques. Protection of reactive groups, such as the acid or alkenyl groups, may be done at any step
- 20 through known techniques, for example alkylation or iodination. Methods used include methylation of the fatty acids to produce methyl esters. Similarly, protecting groups may be removed at any step. Desirably, purification of fractions containing ARA, DHA and EPA is accomplished by treatment with urea and/or fractional distillation.

USES OF FATTY ACIDS

- 25 The uses of the fatty acids of subject invention are several. Probes based on the DNAs of the present invention may find use in methods for isolating related molecules or in methods to detect organisms expressing desaturases. When used as probes, the DNAs or oligonucleotides need to be detectable. This
30 is usually accomplished by attaching a label either at an internal site, for

- example via incorporation of a modified residue, or at the 5' or 3' terminus. Such labels can be directly detectable, can bind to a secondary molecule that is detectably labeled, or can bind to an unlabelled secondary molecule and a detectably labeled tertiary molecule; this process can be extended as long as is practical to achieve a satisfactorily detectable signal without unacceptable levels of background signal. Secondary, tertiary, or bridging systems can include use of antibodies directed against any other molecule, including labels or other antibodies, or can involve any molecules which bind to each other, for example a biotin-streptavidin/avidin system. Detectable labels typically include radioactive isotopes, molecules which chemically or enzymatically produce or alter light, enzymes which produce detectable reaction products, magnetic molecules, fluorescent molecules or molecules whose fluorescence or light-emitting characteristics change upon binding. Examples of labelling methods can be found in USPN 5,011,770. Alternatively, the binding of target molecules can be directly detected by measuring the change in heat of solution on binding of probe to target via isothermal titration calorimetry, or by coating the probe or target on a surface and detecting the change in scattering of light from the surface produced by binding of target or probe, respectively, as may be done with the BIACore system.
- PUFAs of the subject invention produced by recombinant means find applications in a wide variety of areas. Supplementation of humans or animals with PUFAs in various forms can result in increased levels not only of the added PUFAs, but of their metabolic progeny as well. For example, where the inherent $\Delta 6$ -desaturase pathway is dysfunctional in an individual, treatment with GLA can result not only in increased levels of GLA, but also of downstream products such as ARA and prostaglandins (see Figure 1). Complex regulatory mechanisms can make it desirable to combine various PUFAs, or to add different conjugates of PUFAs, in order to prevent, control or overcome such mechanisms to achieve the desired levels of specific PUFAs in an individual.
- PUFAs, or derivatives thereof, made by the disclosed method can be used as dietary supplements, particularly in infant formulas, for patients

undergoing intravenous feeding or for preventing or treating malnutrition. Particular fatty acids such as EPA are used to alter the composition of infant formulas to better replicate the PUFA composition of human breast milk. The predominant triglyceride in human milk has been reported to be 1,3-di-oleoyl-2-palmitoyl, with 2-palmitoyl glycerides reported as better absorbed than 2-oleoyl or 2-linoleoyl glycerides (USPN 4,876,107). Typically, human breast milk has a fatty acid profile comprising from about 0.15 % to about 0.36 % as DHA, from about 0.03 % to about 0.13 % as EPA, from about 0.30 % to about 0.88 % as ARA, from about 0.22 % to about 0.67 % as DGLA, and from about 0.27 % to about 1.04 % as GLA. A preferred ratio of GLA:DGLA:ARA in infant formulas is from about 1:1:4 to about 1:1:1, respectively. Amounts of oils providing these ratios of PUFA can be determined without undue experimentation by one of skill in the art. PUFAs, or host cells containing them, also can be used as animal food supplements to alter an animal's tissue or milk fatty acid composition to one more desirable for human or animal consumption.

NUTRITIONAL COMPOSITIONS

The present invention also includes nutritional compositions. Such compositions, for purposes of the present invention, include any food or preparation for human consumption including for enteral or parenteral consumption, which when taken into the body (a) serve to nourish or build up tissues or supply energy and/or (b) maintain, restore or support adequate nutritional status or metabolic function.

The nutritional composition of the present invention comprises at least one oil or acid produced in accordance with the present invention and may either be in a solid or liquid form. Additionally, the composition may include edible macronutrients, vitamins and minerals in amounts desired for a particular use. The amount of such ingredients will vary depending on whether the composition is intended for use with normal, healthy infants, children or adults having specialized needs such as those which accompany certain metabolic conditions (e.g., metabolic disorders).

Examples of macronutrients which may be added to the composition include but are not limited to edible fats, carbohydrates and proteins. Examples of such edible fats include but are not limited to coconut oil, soy oil, and mono- and diglycerides. Examples of such carbohydrates include but are not limited to glucose, edible lactose and hydrolyzed starch. Additionally, examples of proteins which may be utilized in the nutritional composition of the invention include but are not limited to soy proteins, electrodialysed whey, electrodialysed skim milk, milk whey, or the hydrolysates of these proteins.

With respect to vitamins and minerals, the following may be added to the nutritional compositions of the present invention: calcium, phosphorus, potassium, sodium, chloride, magnesium, manganese, iron, copper, zinc, selenium, iodine, and Vitamins A, E, D, C, and the B complex. Other such vitamins and minerals may also be added.

The components utilized in the nutritional compositions of the present invention will be of semi-purified or purified origin. By semi-purified or purified is meant a material which has been prepared by purification of a natural material or by synthesis.

Examples of nutritional compositions of the present invention include but are not limited to infant formulas, dietary supplements, and rehydration compositions. Nutritional compositions of particular interest include but are not limited to those utilized for enteral and parenteral supplementation for infants, specialist infant formulae, supplements for the elderly, and supplements for those with gastrointestinal difficulties and/or malabsorption.

Nutritional Compositions

A typical nutritional composition of the present invention will contain edible macronutrients, vitamins and minerals in amounts desired for a particular use. The amounts of such ingredients will vary depending on whether the formulation is intended for use with normal, healthy individuals temporarily exposed to stress, or to subjects having specialized needs due to certain chronic or acute disease states (e.g., metabolic disorders). It will be understood by

persons skilled in the art that the components utilized in a nutritional formulation of the present invention are of semi-purified or purified origin. By semi-purified or purified is meant a material that has been prepared by purification of a natural material or by synthesis. These techniques are well known in the art (See, e.g., Code of Federal Regulations for Food Ingredients and Food Processing; Recommended Dietary Allowances, 10th Ed., National Academy Press, Washington, D.C., 1989).

In a preferred embodiment, a nutritional formulation of the present invention is an enteral nutritional product, more preferably an adult or child enteral nutritional product. Accordingly in a further aspect of the invention, a nutritional formulation is provided that is suitable for feeding adults or children who are experiencing stress. The formula comprises, in addition to the PUFAs of the invention; macronutrients, vitamins and minerals in amounts designed to provide the daily nutritional requirements of adults.

The macronutritional components include edible fats, carbohydrates and proteins. Exemplary edible fats are coconut oil, soy oil, and mono- and diglycerides and the PUFA oils of this invention. Exemplary carbohydrates are glucose, edible lactose and hydrolyzed cornstarch. A typical protein source would be soy protein, electrodialysed whey or electrodialysed skim milk or milk whey, or the hydrolysates of these proteins, although other protein sources are also available and may be used. These macronutrients would be added in the form of commonly accepted nutritional compounds in amount equivalent to those present in human milk or an energy basis, i.e., on a per calorie basis.

Methods for formulating liquid and enteral nutritional formulas are well known in the art and are described in detail in the examples.

The enteral formula can be sterilized and subsequently utilized on a ready-to-feed (RTF) basis or stored in a concentrated liquid or a powder. The powder can be prepared by spray drying the enteral formula prepared as indicated above, and the formula can be reconstituted by rehydrating the concentrate. Adult and infant nutritional formulas are well known in the art and commercially available (e.g., Similac®, Ensure®, Jevity® and Alimentum®

from Ross Products Division, Abbott Laboratories). An oil or acid of the present invention can be added to any of these formulas in the amounts described below.

- 5 The energy density of the nutritional composition when in liquid form, can typically range from about 0.6 Kcal to 3 Kcal per ml. When in solid or powdered form, the nutritional supplement can contain from about 1.2 to more than 9 Kcals per gm, preferably 3 to 7 Kcals per gm. In general, the osmolality of a liquid product should be less than 700 mOsm and more preferably less than 660 mOsm.
- 10 The nutritional formula would typically include vitamins and minerals, in addition to the PUFAs of the invention, in order to help the individual ingest the minimum daily requirements for these substances. In addition to the PUFAs listed above, it may also be desirable to supplement the nutritional composition with zinc, copper, and folic acid in addition to antioxidants. It is believed that 15 these substances will also provide a boost to the stressed immune system and thus will provide further benefits to the individual. The presence of zinc, copper or folic acid is optional and is not required in order to gain the beneficial effects on immune suppression. Likewise a pharmaceutical composition can be supplemented with these same substances as well.
- 20 In a more preferred embodiment, the nutritional contains, in addition to the antioxidant system and the PUFA component, a source of carbohydrate wherein at least 5 weight % of said carbohydrate is an indigestible oligosaccharide. In yet a more preferred embodiment, the nutritional composition additionally contains protein, taurine and carnitine.
- 25 The PUFAs, or derivatives thereof, made by the disclosed method can be used as dietary substitutes, or supplements, particularly infant formulas, for patients undergoing intravenous feeding or for preventing or treating malnutrition. Typically, human breast milk has a fatty acid profile comprising from about 0.15 % to about 0.36 % as DHA, from about 0.03 % to about 0.13 % 30 as EPA, from about 0.30 % to about 0.88 % as ARA, from about 0.22 % to about 0.67 % as DGLA, and from about 0.27 % to about 1.04 % as GLA.

Additionally, the predominant triglyceride in human milk has been reported to be 1,3-di-oleoyl-2-palmitoyl, with 2-palmitoyl glycerides reported as better absorbed than 2-oleoyl or 2-linoleoyl glycerides (USPN 4,876,107). Thus, fatty acids such as ARA, DGLA, GLA and/or EPA produced by the invention can be used to alter the composition of infant formulas to better replicate the PUFA composition of human breast milk. In particular, an oil composition for use in a pharmacologic or food supplement, particularly a breast milk substitute or supplement, will preferably comprise one or more of ARA, DGLA and GLA. More preferably the oil will comprise from about 0.3 to 30% ARA, from about 0.2 to 30% DGLA, and from about 0.2 to about 30% GLA.

In addition to the concentration, the ratios of ARA, DGLA and GLA can be adapted for a particular given end use. When formulated as a breast milk supplement or substitute, an oil composition which contains two or more of ARA, DGLA and GLA will be provided in a ratio of about 1:19:30 to about 6:1:0.2, respectively. For example, the breast milk of animals can vary in ratios of ARA:DGLA:DGL ranging from 1:19:30 to 6:1:0.2, which includes intermediate ratios which are preferably about 1:1:1, 1:2:1, 1:1:4. When produced together in a host cell, adjusting the rate and percent of conversion of a precursor substrate such as GLA and DGLA to ARA can be used to precisely control the PUFA ratios. For example, a 5% to 10% conversion rate of DGLA to ARA can be used to produce an ARA to DGLA ratio of about 1:19, whereas a conversion rate of about 75% to 80% can be used to produce an ARA to DGLA ratio of about 6:1. Therefore, whether in a cell culture system or in a host animal, regulating the timing, extent and specificity of desaturase expression as described can be used to modulate the PUFA levels and ratios. Depending on the expression system used, e.g., cell culture or an animal expressing oil(s) in its milk, the oils also can be isolated and recombined in the desired concentrations and ratios. Amounts of oils providing these ratios of PUFA can be determined following standard protocols. PUFAs, or host cells containing them, also can be used as animal food supplements to alter an animal's tissue or milk fatty acid composition to one more desirable for human or animal consumption.

For dietary supplementation, the purified PUFAs, or derivatives thereof, may be incorporated into cooking oils, fats or margarines formulated so that in normal use the recipient would receive the desired amount. The PUFAs may also be incorporated into infant formulas, nutritional supplements or other food products, and may find use as anti-inflammatory or cholesterol lowering agents.

Pharmaceutical Compositions

The present invention also encompasses a pharmaceutical composition comprising one or more of the acids and/or resulting oils produced in accordance with the methods described herein. More specifically, such a pharmaceutical composition may comprise one or more of the acids and/or oils as well as a standard, well-known, non-toxic pharmaceutically acceptable carrier, adjuvant or vehicle such as, for example, phosphate buffered saline, water, ethanol, polyols, vegetable oils, a wetting agent or an emulsion such as a water/oil emulsion. The composition may be in either a liquid or solid form.

For example, the composition may be in the form of a tablet, capsule, ingestible liquid or powder, injectible, or topical ointment or cream.

Possible routes of administration include, for example, oral, rectal and parenteral. The route of administration will, of course, depend upon the desired effect. For example, if the composition is being utilized to treat rough, dry, or aging skin, to treat injured or burned skin, or to treat skin or hair affected by a disease or condition, it may perhaps be applied topically.

The dosage of the composition to be administered to the patient may be determined by one of ordinary skill in the art and depends upon various factors such as weight of the patient, age of the patient, immune status of the patient, etc.

With respect to form, the composition may be, for example, a solution, a dispersion, a suspension, an emulsion or a sterile powder which is then reconstituted.

Additionally, the composition of the present invention may be utilized for cosmetic purposes. It may be added to pre-existing cosmetic compositions such that a mixture is formed or may be used as a sole composition.

Pharmaceutical compositions may be utilized to administer the PUFA component to an individual. Suitable pharmaceutical compositions may comprise physiologically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions and sterile powders for reconstitution into sterile solutions or dispersions for ingestion. Examples of suitable aqueous and non-aqueous carriers, diluents, solvents or vehicles include water, ethanol, polyols (propyleneglycol, polyethyleneglycol, glycerol, and the like), suitable mixtures thereof, vegetable oils (such as olive oil) and injectable organic esters such as ethyl oleate. Proper fluidity can be maintained, for example, by the maintenance of the required particle size in the case of dispersions and by the use of surfactants. It may also be desirable to include isotonic agents, for example sugars, sodium chloride and the like. Besides such inert diluents, the composition can also include adjuvants, such as wetting agents, emulsifying and suspending agents, sweetening, flavoring and perfuming agents.

Suspensions, in addition to the active compounds, may contain suspending agents, as for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth or mixtures of these substances, and the like.

Solid dosage forms such as tablets and capsules can be prepared using techniques well known in the art. For example, PUFAs of the invention can be tableted with conventional tablet bases such as lactose, sucrose, and cornstarch in combination with binders such as acacia, cornstarch or gelatin, disintegrating agents such as potato starch or alginic acid and a lubricant such as stearic acid or magnesium stearate. Capsules can be prepared by incorporating these excipients into a gelatin capsule along with the antioxidants and the PUFA component. The amount of the antioxidants and PUFA component that should

be incorporated into the pharmaceutical formulation should fit within the guidelines discussed above.

As used in this application, the term "treat" refers to either preventing, or reducing the incidence of, the undesired occurrence. For example, to treat

- 5 immune suppression refers to either preventing the occurrence of this suppression or reducing the amount of such suppression. The terms "patient" and "individual" are being used interchangeably and both refer to an animal. The term "animal" as used in this application refers to any warm-blooded mammal including, but not limited to, dogs, humans, monkeys, and apes. As 10 used in the application the term "about" refers to an amount varying from the stated range or number by a reasonable amount depending upon the context of use. Any numerical number or range specified in the specification should be considered to be modified by the term about.

"Dose" and "serving" are used interchangeably and refer to the amount 15 of the nutritional or pharmaceutical composition ingested by the patient in a single setting and designed to deliver effective amounts of the antioxidants and the structured triglyceride. As will be readily apparent to those skilled in the art, a single dose or serving of the liquid nutritional powder should supply the amount of antioxidants and PUFAs discussed above. The amount of the dose or 20 serving should be a volume that a typical adult can consume in one sitting. This amount can vary widely depending upon the age, weight, sex or medical condition of the patient. However as a general guideline, a single serving or dose of a liquid nutritional produce should be considered as encompassing a volume from 100 to 600 ml, more preferably from 125 to 500 ml and most 25 preferably from 125 to 300 ml.

The PUFAs of the present invention may also be added to food even when supplementation of the diet is not required. For example, the composition may be added to food of any type including but not limited to margarines, modified butters, cheeses, milk, yogurt, chocolate, candy, snacks, salad oils, 30 cooking oils, cooking fats, meats, fish and beverages.

Pharmaceutical Applications

For pharmaceutical use (human or veterinary), the compositions are generally administered orally but can be administered by any route by which they may be successfully absorbed, e.g., parenterally (i.e. subcutaneously, 5 intramuscularly or intravenously), rectally or vaginally or topically, for example, as a skin ointment or lotion. The PUFAs of the present invention may be administered alone or in combination with a pharmaceutically acceptable carrier or excipient. Where available, gelatin capsules are the preferred form of oral administration. Dietary supplementation as set forth above also can 10 provide an oral route of administration. The unsaturated acids of the present invention may be administered in conjugated forms, or as salts, esters, amides or prodrugs of the fatty acids. Any pharmaceutically acceptable salt is encompassed by the present invention; especially preferred are the sodium, potassium or lithium salts. Also encompassed are the N-alkylpolyhydroxamine 15 salts, such as N-methyl glucamine, found in PCT publication WO 96/33155. The preferred esters are the ethyl esters. As solid salts, the PUFAs also can be administered in tablet form. For intravenous administration, the PUFAs or derivatives thereof may be incorporated into commercial formulations such as Intralipids. The typical normal adult plasma fatty acid profile comprises 6.64 to 20 9.46% of ARA, 1.45 to 3.11% of DGLA, and 0.02 to 0.08% of GLA. These PUFAs or their metabolic precursors can be administered, either alone or in mixtures with other PUFAs, to achieve a normal fatty acid profile in a patient. Where desired, the individual components of formulations may be individually 25 provided in kit form, for single or multiple use. A typical dosage of a particular fatty acid is from 0.1 mg to 20 g, or even 100 g daily, and is preferably from 10 mg to 1, 2, 5 or 10 g daily as required, or molar equivalent amounts of derivative forms thereof. Parenteral nutrition compositions comprising from about 2 to about 30 weight percent fatty acids calculated as triglycerides are encompassed by the present invention; preferred is a composition having from 30 about 1 to about 25 weight percent of the total PUFA composition as GLA (USPN 5,196,198). Other vitamins, and particularly fat-soluble vitamins such as vitamin A, D, E and L-carnitine can optionally be included. Where desired, a

preservative such as α tocopherol may be added, typically at about 0.1% by weight.

Suitable pharmaceutical compositions may comprise physiologically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions and sterile powders for reconstitution into sterile injectible solutions or dispersions. Examples of suitable aqueous and non-aqueous carriers, diluents, solvents or vehicles include water, ethanol, polyols (propyleneglyol, polyethyleneglycol, glycerol, and the like), suitable mixtures thereof, vegetable oils (such as olive oil) and injectable organic esters such as ethyl oleate. Proper fluidity can be maintained, for example, by the maintenance of the required particle size in the case of dispersions and by the use of surfactants. It may also be desirable to include isotonic agents, for example sugars, sodium chloride and the like. Besides such inert diluents, the composition can also include adjuvants, such as wetting agents, emulsifying and suspending agents, sweetening, flavoring and perfuming agents.

Suspensions in addition to the active compounds, may contain suspending agents, as for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth, or mixtures of these substances and the like.

An especially preferred pharmaceutical composition contains diacetyltauric acid esters of mono- and diglycerides dissolved in an aqueous medium or solvent. Diacetyltauric acid esters of mono- and diglycerides have an HLB value of about 9-12 and are significantly more hydrophilic than existing antimicrobial lipids that have HLB values of 2-4. Those existing hydrophobic lipids cannot be formulated into aqueous compositions. As disclosed herein, those lipids can now be solubilized into aqueous media in combination with diacetyltauric acid esters of mono-and diglycerides. In accordance with this embodiment, diacetyltauric acid esters of mono- and diglycerides (e.g., DATEM-C12:0) is melted with other active antimicrobial lipids (e.g., 18:2 and 12:0 monoglycerides) and mixed to obtain a homogeneous mixture.

Homogeneity allows for increased antimicrobial activity. The mixture can be completely dispersed in water. This is not possible without the addition of diacetyl tartaric acid esters of mono- and diglycerides and premixing with other monoglycerides prior to introduction into water. The aqueous composition can

- 5 then be admixed under sterile conditions with physiologically acceptable diluents, preservatives, buffers or propellants as may be required to form a spray or inhalant.

The present invention also encompasses the treatment of numerous disorders with fatty acids. Supplementation with PUFAs of the present
10 invention can be used to treat restenosis after angioplasty. Symptoms of inflammation, rheumatoid arthritis, and asthma and psoriasis can be treated with the PUFAs of the present invention. Evidence indicates that PUFAs may be involved in calcium metabolism, suggesting that PUFAs of the present invention may be used in the treatment or prevention of osteoporosis and of
15 kidney or urinary tract stones.

The PUFAs of the present invention can be used in the treatment of cancer. Malignant cells have been shown to have altered fatty acid compositions; addition of fatty acids has been shown to slow their growth and cause cell death, and to increase their susceptibility to chemotherapeutic agents.
20 GLA has been shown to cause reexpression on cancer cells of the E-cadherin cellular adhesion molecules, loss of which is associated with aggressive metastasis. Clinical testing of intravenous administration of the water soluble lithium salt of GLA to pancreatic cancer patients produced statistically significant increases in their survival. PUFA supplementation may also be
25 useful for treating cachexia associated with cancer.

The PUFAs of the present invention can also be used to treat diabetes (USPN 4,826,877; Horrobin *et al.*, Am. J. Clin. Nutr. Vol. 57 (Suppl.), 732S-737S). Altered fatty acid metabolism and composition has been demonstrated in diabetic animals. These alterations have been suggested to be involved in
30 some of the long-term complications resulting from diabetes, including retinopathy, neuropathy, nephropathy and reproductive system damage.

Primrose oil, which contains GLA, has been shown to prevent and reverse diabetic nerve damage.

The PUFAs of the present invention can be used to treat eczema, reduce blood pressure and improve math scores. Essential fatty acid deficiency has

5 been suggested as being involved in eczema, and studies have shown beneficial effects on eczema from treatment with GLA. GLA has also been shown to reduce increases in blood pressure associated with stress, and to improve performance on arithmetic tests. GLA and DGLA have been shown to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels and inhibit

10 proliferation of vessel wall smooth muscle and fibrous tissue (Brenner *et al.*, Adv. Exp. Med. Biol. Vol. 83, p. 85-101, 1976). Administration of GLA or DGLA, alone or in combination with EPA, has been shown to reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs (USPN 4,666,701). GLA and DGLA have also been shown

15 to prevent or treat endometriosis and premenstrual syndrome (USPN 4,758,592) and to treat myalgic encephalomyelitis and chronic fatigue after viral infections (USPN 5,116,871).

Further uses of the PUFAs of this invention include use in treatment of AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and

20 inflammatory skin disorders. The PUFAs of the inventions also can be used for formulas for general health as well as for geriatric treatments.

Veterinary Applications

It should be noted that the above-described pharmaceutical and nutritional compositions may be utilized in connection with animals, as well as

25 humans, as animals experience many of the same needs and conditions as human. For example, the oil or acids of the present invention may be utilized in animal feed supplements or as animal feed substitutes.

The following examples are presented by way of illustration, not of limitation.

- Examples**
- Example 1 Isolation of $\Delta 5$ Desaturase Nucleotide Sequence from
Mortierella alpina
- 5 Example 2 Isolation of $\Delta 6$ Desaturase Nucleotide Sequence from
Mortierella alpina
- Example 3 Identification of $\Delta 6$ Desaturases Homologues to the
Mortierella alpina Δ Desaturase
- 10 Example 4 Isolation of D-12 Desaturase Nucleotide Sequence from
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Sequence from *Mortierella alpina*
- 15 Example 6 Expression of *M. alpina* Desaturase Clones in Baker's
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- Example 13 Stereospecific Distribution of $\Delta 6$ -Desaturated Oils
- Example 14 Fatty Acid Compositions of Transgenic Plants

Example 15 Combined Expression of $\Delta 6$ and $\Delta 12$ Desaturases in *B. napus* Achieved by Crossing

Example 16 Expression of *M. alpina* desaturases in soybean

Example 17 Human Desaturase Gene Sequences

5

Example 1

Isolation of a $\Delta 5$ -desaturase Nucleotide Sequence from *Mortierella alpina*

Mortierella alpina produces arachidonic acid (ARA, 20:4) from the precursor 20:3 by a $\Delta 5$ -desaturase. A nucleotide sequence encoding the $\Delta 5$ -desaturase from *Mortierella alpina* (see Figure 7) was obtained through PCR

10 amplification using *M. alpina* 1st strand cDNA and degenerate oligonucleotide primers corresponding to amino acid sequences conserved between $\Delta 6$ -desaturases from *Synechocystis* and *Spirulina*. The procedure used was as follows:

Total RNA was isolated from a 3 day old PUFA-producing culture of
15 *Mortierella alpina* using the protocol of Hoge *et al.* (1982) *Experimental Mycology* 6:225-232. The RNA was used to prepare double-stranded cDNA using BRL's lambda-ZipLox system, following the manufacturer's instructions. Several size fractions of the *M. alpina* cDNA were packaged separately to yield libraries with different average-sized inserts. The "full-length" library contains
20 approximately 3×10^6 clones with an average insert size of 1.77 kb. The "sequencing-grade" library contains approximately 6×10^5 clones with an average insert size of 1.1 kb.

5 μ g of total RNA was reverse transcribed using BRL Superscript RTase and the primer TSyn 5'-CAAGCTTCTGCAGGAGCTTTTTTTTTTT-
25 3' (SEQ ID NO:19.) Degenerate oligonucleotides were designed to regions conserved between the two cyanobacterial $\Delta 6$ -desaturase sequences. The specific primers used were:

D6DESAT-F3 (SEQ ID NO:20)

5'-CUACUACUACUACAYCAYACOTAYACOOAYAT-3'

D6DESAT-R3 (SEQ ID NO:21)

5'-CAUCAUCAUOGGRAAOARRTGRTG-3'

5 where Y=C+T, R=A+G, and O=I+C. PCR amplification was carried out in a 25 μ l volume containing: template derived from 40 ng total RNA, 2 pM each primer, 200 μ M each deoxyribonucleotide triphosphate, 60 mM Tris-Cl, pH 8.5, 15 mM (NH₄)₂SO₄, 2 mM MgCl₂. Samples were subjected to an initial desaturation step of 95 degrees (all temperatures Celsius) for 5 minutes, then 10 held at 72 degrees while 0.2 U of Taq polymerase were added. PCR thermocycling conditions were as follows: 94 degrees for 1 min., 45 degrees for 1.5 min., 72 degrees for 2 min. PCR was continued for 35 cycles. PCR using these primers on the *M. alpina* first-strand cDNA produced a 550 bp reaction product. Comparison of the deduced amino acid sequence of the *M.* 15 *alpina* PCR fragment revealed regions of homology with Δ 6-desaturases (see Figure 4). However, there was only about 28% identity over the region compared. The deduced amino acid sequence is presented in SEQ ID NO:14.

The PCR product was used as a probe to isolate corresponding cDNA clones from a *M. alpina* library. The longest cDNA clone, Ma29, was 20 designated pCGN5521 and has been completely sequenced on both strands. The cDNA is contained as a 1481 bp insert in the vector pZL1 (Bethesda Research Laboratories) and, beginning with the first ATG, contains an open reading frame encoding 446 amino acids. The reading frame contains the sequence deduced from the PCR fragment. The sequence of the cDNA insert 25 was found to contain regions of homology to Δ 6-desaturases (see Figure 8). For example, three conserved "histidine boxes" (that have been observed in other membrane-bound desaturases (Okuley *et al.*, (1994) *The Plant Cell* 6:147-158)) were found to be present in the *Mortierella* sequence at amino acid positions 171-175, 207-212, and 387-391 (see Figure 5A-5D). However, the typical 30 "HXXHH" amino acid motif for the third histidine box for the *Mortierella*

desaturase was found to be QXXHH. The amino-terminus of the encoded protein, showed significant homology to cytochrome b5 proteins. Thus, the *Mortierella* cDNA clone appears to represent a fusion between a cytochrome b5 and a fatty acid desaturase. Since cytochrome b5 is believed to function as the 5 electron donor for membrane-bound desaturase enzymes, it is possible that the N-terminal cytochrome b5 domain of this desaturase protein is involved in its function. This may be advantageous when expressing the desaturase in heterologous systems for PUFA production.

Example 2

10 **Isolation of Δ6 Desaturase Nucleotide Sequence from *Mortierella alpina***

A nucleic acid sequence from a partial cDNA clone, Ma524, encoding a Δ6 fatty acid desaturase from *Mortierella alpina* was obtained by random sequencing of clones from the *M. alpina* cDNA library described in Example 1. cDNA-containing plasmids were excised as follows:

15 Five μl of phage were combined with 100 μl of *E. coli* DH10B(ZIP) grown in ECLB plus 10 μg/ml kanamycin, 0.2% maltose, and 10 mM MgSO₄ and incubated at 37 degrees for 15 minutes. 0.9 ml SOC was added and 100 μl of the bacteria immediately plated on each of 10 ECLB + 50 μg Pen plates. No 45 minute recovery time was needed. The plates were incubated overnight at 37
20 degrees. Colonies were picked into ECLB + 50 μg Pen media for overnight cultures to be used for making glycerol stocks and miniprep DNA. An aliquot of the culture used for the miniprep is stored as a glycerol stock. Plating on ECLB + 50 μg Pen/ml resulted in more colonies and a greater proportion of colonies containing inserts than plating on 100 μg/ml Pen.

25 Random colonies were picked and plasmid DNA purified using Qiagen miniprep kits. DNA sequence was obtained from the 5' end of the cDNA insert and compared to the databases using the BLAST algorithm. Ma524 was identified as a putative Δ6 desaturase based on DNA sequence homology to previously identified Δ6 desaturases. A full-length cDNA clone was isolated

from the *M. alpina* library. The abundance of this clone appears to be slightly (2X) less than Ma29. Ma524 displays significant homology to a portion of a *Caenorhabditis elegans* cosmid, WO6D2.4, a cytochrome b5/desaturase fusion protein from sunflower, and the two Δ6 desaturases in the public databanks
5 those from *Synechocystis* and *Spirulina*.

In addition, Ma524 shows significant homology to the borage Δ6-desaturase sequence (PCT publication WO 96/21022). Ma524 thus appears to encode a Δ6-desaturase that is related to the borage and algal Δ6-desaturases. It should be noted that, although the amino acid sequences of Ma524 and the
10 borage Δ6 are similar, the base composition of the cDNAs is quite different: the borage cDNA has an overall base composition of 60 % A+T, with some regions exceeding 70 %, while Ma524 has an average of 44 % A+T base composition, with no regions exceeding 60 %. This may have implications for expressing the cDNAs in microorganisms or animals which favor different base compositions.
15 It is known that poor expression of recombinant genes can occur when the host has a very different base composition from that of the introduced gene. Speculated mechanisms for such poor expression include decreased stability or translatability of the mRNA.

Example 3

20 Identification of Δ6-desaturases Homologous
 to the *Mortierella alpina* Δ6-desaturase

Nucleic acid sequences that encode putative Δ6-desaturases were identified through a BLASTX search of the est databases through NCBI using the Ma524 amino acid sequence. Several sequences showed significant
25 homology. In particular, the deduced amino acid sequence of two *Arabidopsis thaliana* sequences, (accession numbers F13728 and T42806) showed homology to two different regions of the deduced amino acid sequence of Ma524. The following PCR primers were designed: ATTS4723-FOR (complementary to F13728) 5'-CUACUACUACUAGGAGTCCTCTA
30 CGGTGTTTG, SEQ ID NO:22, and T42806-REV (complementary to

T42806) 5' CAUCAUCAUCAUATGATGCTCAAGCTGAACTG, SEQ ID NO:23. Five µg of total RNA isolated from developing siliques of *Arabidopsis thaliana* was reverse transcribed using BRL Superscript RTase and the primer TSyn 5'-CCAAGCTTCTGCAGGAGCTTTTTTTTTTT-3', (SEQ ID NO:24). PCR was carried out in a 50 ul volume containing: template derived from 25 ng total RNA, 2 pM each primer, 200 µM each deoxyribonucleotide triphosphate, 60 mM Tris-Cl, pH 8.5, 15 mM (NH₄)₂SO₄, 2 mM MgCl₂, 0.2 U Taq Polymerase. Cycle conditions were as follows: 94 degrees for 30 sec., 50 degrees for 30 sec., 72 degrees for 30 sec. PCR was continued for 35 cycles followed by an additional extension at 72 degrees for 7 minutes. PCR resulted in a fragment of ~750 base pairs which was subsequently subcloned, named 12-5, and sequenced. Each end of this fragment corresponds to the *Arabidopsis* est from which the PCR primers were derived. This is the sequence named 12-5. The deduced amino acid sequence of 12-5 is compared to that of Ma524 and ests from human (W28140), mouse (W53753), and *C. elegans* (R05219) in Figure 4. Based on homology, these sequences represent desaturase polypeptides. The full-length genes can be cloned using probes based on the est sequences. The genes can then be placed in expression vectors and expressed in host cells and their specific Δ6- or other desaturase activity can be determined as described below.

Example 4

Isolation of Δ-12 Desaturase Nucleotide Sequence from *Mortierella alpina*

Based on the fatty acids it accumulates, *Mortierella alpina* has an ω6 type desaturase. The ω6 desaturase is responsible for the production of linoleic acid (18:2) from oleic acid (18:1). Linoleic acid (18:2) is a substrate for a Δ6 desaturase. This experiment was designed to determine if *Mortierella alpina* has a Δ12-desaturase polypeptide, and if so, to identify the corresponding nucleotide sequence. A random colony from the *M. alpina* sequencing grade library, Ma648, was sequenced and identified as a putative desaturase based on DNA sequence homology to previously identified desaturases, as described for

Ma524 (*see Example 2*). The deduced amino acid sequence from the 5' end of the Ma648 cDNA displays significant homology to soybean microsomal ω 6 (Δ 12) desaturase (accession #L43921) as well as castor bean oleate 12-hydroxylase (accession #U22378). In addition, homology is observed to a variety of other ω 6 (Δ 12) and ω 3 (Δ 15) fatty acid desaturase sequences.

Example 5

Isolation of Cytochrome b5 Reductase Nucleotide Sequence from *Mortierella alpina*

A nucleic acid sequence encoding a cytochrome b5 reductase from 10 *Mortierella alpina* was obtained as follows. A cDNA library was constructed based on total RNA isolated from *Mortierella alpina* as described in Example 1. DNA sequence was obtained from the 5' and 3' ends of one of the clones, M12-27. A search of public databanks with the deduced amino acid sequence of the 3' end of M12-27 (*see Figure 5*) revealed significant homology to known 15 cytochrome b5 reductase sequences. Specifically, over a 49 amino acid region, the *Mortierella* clone shares 55% identity (73% homology) with a cytochrome b5 reductase from pig (*see Figure 4*).

Example 6

Expression of *M. alpina* Desaturase Clones in Baker's Yeast

Yeast Transformation

Lithium acetate transformation of yeast was performed according to standard protocols (*Methods in Enzymology*, Vol. 194, p. 186-187, 1991). Briefly, yeast were grown in YPD at 30°C. Cells were spun down, resuspended in TE, spun down again, resuspended in TE containing 100 mM lithium acetate, 25 spun down again, and resuspended in TE/lithium acetate. The resuspended yeast were incubated at 30°C for 60 minutes with shaking. Carrier DNA was added, and the yeast were aliquoted into tubes. Transforming DNA was added, and the tubes were incubated for 30 min. at 30°C. PEG solution (35% (w/v) PEG 4000, 100 mM lithium acetate, TE pH7.5) was added followed by a 50

min. incubation at 30°C. A 5 min. heat shock at 42°C was performed, the cells were pelleted, washed with TE, pelleted again and resuspended in TE. The resuspended cells were then plated on selective media.

Desaturase Expression in Transformed Yeast

5 cDNA clones from *Mortierella alpina* were screened for desaturase activity in baker's yeast. A canola Δ15-desaturase (obtained by PCR using 1st strand cDNA from *Brassica napus* cultivar 212/86 seeds using primers based on the published sequence (Arondel *et al. Science* 258:1353-1355)) was used as a positive control. The Δ15-desaturase gene and the gene from cDNA clone
10 Ma29 was put in the expression vector pYES2 (Invitrogen), resulting in plasmids pCGR-2 and pCGR-4, respectively. These plasmids were transfected into *S. cerevisiae* yeast strain 334 and expressed after induction with galactose and in the presence of substrates that allowed detection of specific desaturase activity. The control strain was *S. cerevisiae* strain 334 containing the unaltered
15 pYES2 vector. The substrates used, the products produced and the indicated desaturase activity were: DGLA (conversion to ARA would indicate Δ5-desaturase activity), linoleic acid (conversion to GLA would indicate Δ6-desaturase activity; conversion to ALA would indicate Δ15-desaturase activity), oleic acid (an endogenous substrate made by *S. cerevisiae*, conversion to
20 linoleic acid would indicate Δ12-desaturase activity, which *S. cerevisiae* lacks), or ARA (conversion to EPA would indicate Δ17-desaturase activity). The results are provided in Table 1 below. The lipid fractions were extracted as follows: Cultures were grown for 48-52 hours at 15°C. Cells were pelleted by centrifugation, washed once with sterile ddH₂O, and repelleted. Pellets were
25 vortexed with methanol; chloroform was added along with tritidecanoin (as an internal standard). The mixtures were incubated for at least one hour at room temperature or at 4°C overnight. The chloroform layer was extracted and filtered through a Whatman filter with one gram of anhydrous sodium sulfate to remove particulates and residual water. The organic solvents were evaporated
30 at 40°C under a stream of nitrogen. The extracted lipids were then derivatized to fatty acid methyl esters (FAME) for gas chromatography analysis (GC) by

adding 2 ml of 0.5 N potassium hydroxide in methanol to a closed tube. The samples were heated to 95°C to 100°C for 30 minutes and cooled to room temperature. Approximately 2 ml of 14 % boron trifluoride in methanol was added and the heating repeated. After the extracted lipid mixture cooled, 2 ml
5 of water and 1 ml of hexane were added to extract the FAME for analysis by GC. The percent conversion was calculated by dividing the product produced by the sum of (the product produced and the substrate added) and then multiplying by 100. To calculate the oleic acid percent conversion, as no substrate was added, the total linoleic acid produced was divided by the sum of
10 (oleic acid and linoleic acid produced), then multiplying by 100.

Table 1*M. alpina Desaturase Expression in Baker's Yeast*

CLONE	TYPE OF ENZYME ACTIVITY	% CONVERSION OF SUBSTRATE
pCGR-2 (canola Δ15 desaturase)	Δ6	0 (18:2 to 18:3ω6)
	Δ15	16.3 (18:2 to 18:3ω3)
	Δ5	2.0 (20:3 to 20:4ω6)
	Δ17	2.8 (20:4 to 20:5ω3)
	Δ12	1.8 (18:1 to 18:2ω6)
pCGR-4 (M. alpina Δ6-like, Ma29)	Δ6	0
	Δ15	0
	Δ5	15.3
	Δ17	0.3
	Δ12	3.3
pCGR-7 (M. alpina Δ12-like, Ma648)	Δ6	0
	Δ15	3.8
	Δ5	2.2
	Δ17	0
	Δ12	63.4

The Δ15-desaturase control clone exhibited 16.3% conversion of the substrate. The pCGR-4 clone expressing the Ma29 cDNA converted 15.3% of the 20:3 substrate to 20:4ω6, indicating that the gene encodes a Δ5-desaturase. The background (non-specific conversion of substrate) was between 0-3% in these cases. The pCGR-5 clone expressing the Ma524 cDNA showed 6% conversion of the substrate to GLA, indicating that the gene encodes a Δ6-desaturase. The pCGR-7 clone expressing the Ma648 cDNA converted 63.4% conversion of the substrate to LA, indicating that the gene encodes a Δ12-desaturase. Substrate inhibition of activity was observed by using different concentrations of the substrate. When substrate was added to 100 μM, the percent conversion to product dropped as compared to when substrate was added to 25 μM (see below). These data show that desaturases with different

substrate specificities can be expressed in a heterologous system and used to produce PUFAs.

Table 2 represents fatty acids of interest as a percent of the total lipid extracted from the yeast host *S. cerevisiae* 334 with the indicated plasmid. No glucose was present in the growth media. Affinity gas chromatography was used to separate the respective lipids. GC/MS was employed to verify the identity of the product(s). The expected product for the *B. napus* $\Delta 15$ -desaturase, α -linolenic acid, was detected when its substrate, linoleic acid, was added exogenously to the induced yeast culture. This finding demonstrates that yeast expression of a desaturase gene can produce functional enzyme and detectable amounts of product under the current growth conditions. Both exogenously added substrates were taken up by yeast, although slightly less of the longer chain PUFA, dihomo- γ -linolenic acid (20:3), was incorporated into yeast than linoleic acid (18:2) when either was added in free form to the induced yeast cultures. γ -linolenic acid was detected when linoleic acid was present during induction and expression of *S. cerevisiae* 334 (pCGR-5). The presence of this PUFA demonstrates $\Delta 6$ -desaturase activity from pCGR-5 (MA524). Linoleic acid, identified in the extracted lipids from expression of *S. cerevisiae* 334 (pCGR-7), classifies the cDNA MA648 from *M. alpina* as the $\Delta 12$ -desaturase.

Table 2
Fatty Acid as a Percentage of Total Lipid Extracted from Yeast

Plasmid in Yeast (enzyme)	18:2 Incorporated	α -18:3 Produced	γ -18:3 Produced	20:3 Incorporated	20:4 Produced	18:1* Present	18:2 Produced
pYES2 (control)	66.9	0	0	58.4	0	4	0
pCGR-2 (Δ 15)	60.1	5.7	0	50.4	0	0.7	0
pCGR-4 (Δ 5)	67	0	0	32.3	5.8	0.8	0
pCGR-5 (Δ 6)	62.4	0	4.0	49.9	0	2.4	0
pCGR-7 (Δ 12)	65.6	0	0	45.7	0	7.1	12.2

100 μ M substrate added

* 18:1 is an endogenous fatty acid in yeast

5**Key To Tables**

18:1 =oleic acid
 18:2 =linoleic acid

α -18:3 = α -linolenic acid
 γ -18:3 = γ -linolenic acid

10 18:4 =stearidonic acid
 20:3 =dihomo- γ -linolenic acid
 20:4 =arachidonic acid

Example 7Expression of Δ5 Desaturase in PlantsExpression in Leaves

This experiment was designed to determine whether leaves expressing
5 Ma29 (as determined by Northern) were able to convert exogenously applied
DGLA (20:3) to ARA (20:4).

The Ma29 desaturase cDNA was modified by PCR to introduce
convenient restriction sites for cloning. The desaturase coding region has been
inserted into a d35 cassette under the control of the double 35S promoter for
10 expression in *Brassica* leaves (pCGN5525) following standard protocols (*see*
USPN 5,424,200 and USPN 5,106,739). Transgenic *Brassica* plants containing
pCGN5525 were generated following standard protocols (*see* USPN 5,188,958
and USPN 5,463,174).

In the first experiment, three plants were used: a control, LP004-1, and
15 two transgenics, 5525-23 and 5525-29. LP004 is a low-linolenic *Brassica*
variety. Leaves of each were selected for one of three treatments: water, GLA
or DGLA. GLA and DGLA were purchased as sodium salts from NuChek Prep
and dissolved in water at 1 mg/ml. Aliquots were capped under N₂ and stored at
-70 degrees C. Leaves were treated by applying a 50 μl drop to the upper
20 surface and gently spreading with a gloved finger to cover the entire surface.
Applications were made approximately 30 minutes before the end of the light
cycle to minimize any photo-oxidation of the applied fatty acids. After 6 days
of treatment one leaf from each treatment was harvested and cut in half through
the mid rib. One half was washed with water to attempt to remove
25 unincorporated fatty acid. Leaf samples were lyophilized overnight, and fatty
acid composition determined by gas chromatography (GC). The results are
shown in Table 3.

Table 3
Fatty Acid Analysis of Leaves from Ma29 Transgenic *Brassica* Plants

Treatment	SPL	16:00	16:01	18:00	18:01	18:10	18:1v	18:02	18:3g	18:03	18:04	20:00	20:01
	#	%	%	%	%	%	%	%	%	%	%	%	%
Water	33	12.95	0.08	2.63	2.51	1.54	0.98	16.76	0	45.52	0	0.09	0
	34	13.00	0.09	2.67	2.56	1.55	1.00	16.86	0	44.59	0	0.15	0
	35	14.13	0.09	2.37	2.15	1.27	0.87	16.71	0	49.91	0	0.05	0.01
	36	13.92	0.08	2.32	2.07	1.21	0.86	16.16	0	50.25	0	0.05	0
	37	13.79	0.11	2.10	2.12	1.26	0.86	15.90	0.08	46.29	0	0.54	0.01
GLA	38	12.80	0.09	1.94	2.08	1.35	0.73	14.54	0.11	45.61	0	0.49	0.01
	39	12.10	0.09	2.37	2.10	1.29	0.82	14.85	1.63	43.66	0	0.53	0
	40	12.78	0.10	2.34	2.22	1.36	0.86	15.29	1.72	47.22	0	0.50	0.02
	41	13.71	0.07	2.68	2.16	1.34	0.82	15.92	2.12	46.55	0	0.09	0
DGLA	42	14.10	0.07	2.75	2.35	1.51	0.84	16.66	1.56	46.41	0	0.09	0.01
	43	13.62	0.09	2.22	1.94	1.21	0.73	14.68	2.42	46.69	0	0.51	0.01
	44	13.92	0.09	2.20	2.17	1.32	0.85	15.22	2.30	46.05	0	0.53	0.02
	45	12.45	0.14	2.30	2.28	1.37	0.91	15.65	0.07	44.62	0	0.12	0.01
	46	12.67	0.15	2.69	2.50	1.58	0.92	15.96	0.09	42.77	0	0.56	0.01
	47	12.56	0.23	3.40	1.98	1.13	0.86	13.57	0.03	45.52	0	0.51	0.01
	48	13.07	0.24	3.60	2.51	1.63	0.88	13.54	0.04	45.13	0	0.50	0.01
	49	13.26	0.07	2.81	2.34	1.67	0.67	16.04	0.04	43.89	0	0.59	0
	50	13.53	0.07	2.84	2.41	1.70	0.70	16.07	0.02	44.90	0	0.60	0.01

Table 3 - Continued
Fatty Acid Analysis of Leaves from Ma29 Transgenic *Brassica* Plants

Treatment	SPL	20:02	20:03	20:04	20:05	22:00	22:01	22:02	22:03	22:06	24:0	24:1
#	%	%	%	%	%	%	%	%	%	%	%	%
Water	33	0	0	0.29	0	0.01	0.09	16.26	0	0	0.38	0.18
	34	0.01	0	0.26	0	0.14	0.10	16.82	0.02	0.05	0.36	0.27
	35	0.01	0	0.25	0	0.12	0.06	11.29	0.04	0.05	0.29	0.25
	36	0	0.01	0.26	0	0.07	0.04	11.82	0.03	0.36	0.28	0.21
	37	0.02	0	0.21	0	0.18	0.08	15.87	0.06	0.20	0.30	0.17
	38	0.01	0	0.24	0	0.15	0.07	13.64	0.09	0.08	5.89	0.23
GLA	39	0.02	0.01	0.27	0	0.10	0.08	16.25	3.42	0.19	0.37	0.17
	40	0.01	0	0.27	0	0.10	0.10	14.74	0.05	0.10	0.36	0.14
	41	0	0	0.27	0	0.20	0.10	13.15	0.13	0.29	0.33	0.20
	42	0	0	0.28	0	0.11	0.11	12.60	0.02	0.24	0.38	0.13
	43	0.01	0	0.28	0	0.10	0.03	14.73	0.01	0.24	0.34	0.14
	44	0.02	0	0.26	0	0.13	0.07	14.43	0.05	0.16	0.33	0.17
DGLA	45	0.06	1.21	0.26	0	0.07	0.07	18.67	0.02	0.21	0.36	0.13
	46	0	1.94	0.27	0	0.11	0.09	17.97	0.09	0.39	0.41	0.11
	47	0.01	0.69	0.96	0	0.11	0.07	17.96	0	0.22	0.49	0.20
	48	0.01	0.70	0.74	0	0.14	0.09	17.14	0.05	0.32	0.52	0.10
	49	0	0.35	1.11	0	0.10	0.07	17.26	0.07	0.23	0.39	0.18
	50	0	0.20	0.87	0	0.21	0.07	15.73	0.04	0.15	0.37	0.18

Leaves treated with GLA contained from 1.56 to 2.4 wt% GLA. The fatty acid analysis showed that the lipid composition of control and transgenic leaves was essentially the same. Leaves of control plants treated with DGLA contained 1.2-1.9 w% DGLA and background amounts of ARA (.26-.27 wt%).

- 5 Transgenic leaves contained only .2-.7 wt% DGLA, but levels of ARA were increased (.74-1.1 wt%) indicating that the DGLA was converted to ARA in these leaves.

Expression in Seed

- 10 The purpose of this experiment was to determine whether a construct with the seed specific napin promoter would enable expression in seed.

The Ma29 cDNA was modified by PCR to introduce *Xho*I cloning sites upstream and downstream of the start and stop codons, respectively, using the following primers:

Madxho-forward:

- 15 5'-CUACUACUACUACTCGAGCAAGATGGAACGGACCAAGG
(SEQ ID NO:25)

Madxho-reverse:

- 5'-CAUCAUCAUCAUCTCGAGCTACTCTCCTTGGGACGGAG
(SEQ ID NO:26).

- 20 The PCR product was subcloned into pAMP1 (GIBCOBRL) using the CloneAmp system (GIBCOBRL) to create pCGN5522 and the Δ5 desaturase sequence was verified by sequencing of both strands.

- 25 For seed-specific expression, the Ma29 coding region was cut out of pCGN5522 as an *Xho*I fragment and inserted into the *Sall* site of the napin expression cassette, pCGN3223, to create pCGN5528. The *Hind*III fragment of pCGN5528 containing the napin 5' regulatory region, the Ma29 coding region, and the napin 3' regulatory region was inserted into the *Hind*III site of pCGN1557 to create pCGN5531. Two copies of the napin transcriptional unit were inserted in tandem. This tandem construct can permit higher expression of

the desaturases per genetic loci. pCGN5531 was introduced into *Brassica napus* cv.LP004 via Agrobacterium mediated transformation.

The fatty acid composition of twenty-seed pools of mature T2 seeds was analyzed by GC. Table 4 shows the results obtained with independent 5 transformed lines as compared to non-transformed LP004 seed. The transgenic seeds containing pCGN5531 contain two fatty acids that are not present in the control seeds, tentatively identified as taxoleic acid (5,9-18:2) and pinolenic acid (5,9,12-18:3), based on their elution relative to oleic and linoleic acid. These would be the expected products of $\Delta 5$ desaturation of oleic and linoleic 10 acids. No other differences in fatty acid composition were observed in the transgenic seeds.

Table 4
Composition of T2 Pooled Seed

	16:0	16:1	18:0	18:1	(5,9)18:2	18:2	(5,9,12)18:3	18:3	20:0	20:1	20:2	22:0	22:1	22:2	24:0
	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%
LP004 control	3.86	0.15	3.05	69.1	0	18.51	0.01	1.65	1.09	1.40	0.03	0.63	0.05	0.42	
5531-1	4.26	0.15	3.23	62.33	4.07	21.44	0.33	1.38	0.91	1.04	0.05	0.41	0.03	0.27	
5531-2	3.78	0.14	3.37	66.18	4.57	17.31	0.27	1.30	1.03	1.18	0	0.47	0.01	0.30	
5531-6	3.78	0.13	3.47	63.61	6.21	17.97	0.38	1.34	1.04	1.14	0.05	0.49	0.02	0.26	
5531-10	3.96	0.17	3.28	63.82	5.41	18.58	0.32	1.43	0.98	1.11	0.02	0.50	0	0.31	
5531-16	3.91	0.17	3.33	64.31	5.03	18.98	0.33	1.39	0.96	1.11	0	0.44	0	0	
5531-28	3.81	0.13	2.58	62.64	5.36	20.95	0.45	1.39	0.83	1.15	0.01	0.36	0.05	0.21	

Northern analysis is performed on plants to identify those expressing Ma29. Developing embryos are isolated approximately 25 days post anthesis or when the napin promoter is induced, and floated in a solution containing GLA or DGLA as described in Example 7. Fatty acid analysis of the embryos is then 5 performed by GC to determine the amount of conversion of DGLA to ARA, following the protocol adapted for leaves in Example 7. The amount of ARA incorporated into triglycerides by endogenous *Brassica* acyltransferases is then evaluated by GC analysis as in Example 7.

Example 8

10 **Expression of *M. alpina* Δ6 Desaturase in *Brassica napus***

The Ma524 cDNA was modified by PCR to introduce cloning sites using the following primers:

Ma524PCR-1 (SEQ ID NO:27)

15 5'-CUACUACUACUATCTAGACTCGAGACCATGGCTGCTGCT
CCAGTGTG

Ma524PCR-2 (SEQ ID NO:28)

5'-CAUCAUCAUCAUAGGCCTCGAGTTACTGCGCCTACCCAT

20 These primers allowed the amplification of the entire coding region and added *Xba*I and *Xho*I sites to the 5'-end and *Xho*I and *Stu*I sites to the 3' end. The PCR product was subcloned into pAMP1 (GIBCOBRL) using the CloneAmp system (GIBCOBRL) to create pCGN5535 and the Δ6 desaturase sequence was verified by sequencing of both strands.

25 For seed-specific expression, the Ma524 coding region was cut out of pCGN5535 as an *Xho*I fragment and inserted into the *Sal*I site of the napin expression cassette, pCGN3223, to create pCGN5536. The *Not*I fragment of pCGN5536 containing the napin 5' regulatory region, the Ma524 coding region, and the napin 3' regulatory region was inserted into the *Not*I site of pCGN1557

to create pCGN5538. pCGN5538 was introduced into *Brassica napus* cv.LP004 via Agrobacterium mediated transformation.

Maturing T2 seeds were collected from 6 independent transformation events in the greenhouse. The fatty acid composition of single seeds was analyzed by GC. Table 5 shows the results of control LP004 seeds and six 5538 lines. All of the 5538 lines except #8 produced seeds containing GLA. Presence of GLA segregated in these seeds as is expected for the T2 selfed seed population. In addition to GLA, the *M. alpina* Δ6 desaturase is capable of producing 18:4 (stearidonic) and another fatty acid believed to be the 6,9-18:2.

The above results show that desaturases with three different substrate specificities can be expressed in a heterologous system and used to produce poly-unsaturated long chain fatty acids. Exemplified were the production of ARA (20:4) from the precursor 20:3 (DGLA), the production of GLA (18:3) from 18:2 substrate, and the conversion of 18:1 substrate to 18:2, which is the precursor for GLA.

Table 5
Fatty Acid Analysis of Seeds from Ma524 Transgenic *Brassica* Plants

SPL	#	16:0	16:1	18:0	18:1	6,9 18:2	18:2	18:3ga	18:3	18:4	20:1	22:0	22:1	24:0	24:1
LPOO4-1	4.33	0.21	3.78	72.49	0	13.97	0	1.7	0	1.34	0.71	0.02	0.58	0.27	
-2	4.01	0.16	3.09	73.59	0	14.36	0.01	1.4	0	1.43	0.66	0.02	0.5	0.2	
-3	4.12	0.19	3.56	70.25	0	17.28	0	1.57	0	1.28	0.5	0.02	0.39	0.2	
-4	4.22	0.2	2.7	70.25	0	17.86	0	1.61	0	1.31	0.53	0.02	0.4	0.24	
-5	4.02	0.16	3.41	72.91	0	14.45	0.01	1.45	0	1.37	0.7	0.02	0.51	0.26	
-6	4.22	0.18	3.23	71.47	0	15.92	0.01	1.52	0	1.32	0.69	0.02	0.51	0.27	
-7	4.1	0.16	3.47	72.06	0	15.23	0	1.52	0	1.32	0.63	0.03	0.49	0.23	
-9	4.01	0.17	3.71	72.98	0	13.97	0.01	1.41	0	1.45	0.74	0.03	0.58	0.23	
-10	4.04	0.16	3.57	70.03	0	17.46	0	1.5	0	1.33	0.61	0.03	0.36	0.24	
5538-1-1	4.61	0.2	3.48	68.12	1.37	10.68	7.48	1.04	0.33	1.19	0.49	0.02	0.33	0.13	
-2	4.61	0.22	3.46	68.84	1.36	10.28	7.04	1.01	0.31	1.15	0.48	0.02	0.39	0	
-3	4.78	0.24	3.24	65.86	0	21.36	0	1.49	0	1.08	0.46	0.02	0.38	0.22	
-4	4.84	0.3	3.89	67.64	1.67	9.9	6.97	1.02	0.36	1.14	0.53	0.02	0.5	0.18	
-5	4.64	0.2	3.58	64.5	3.61	8.85	10.14	0.95	0.48	1.19	0.47	0.01	0.33	0.12	
-6	4.91	0.27	3.44	66.51	1.48	11.14	7.74	1.15	0.33	1.08	0.49	0.02	0.34	0.13	
-7	4.87	0.22	3.24	65.78	1.27	11.92	8.38	1.2	0	1.12	0.47	0.02	0.37	0.16	

Table 5
Fatty Acid Analysis of Seeds from Ma524 Transgenic Brassica Plants

SPL #	16:0	16:1	18:0	18:1	6,9 18:2	18:2	18:3ga	18:3	18:4	20:1	22:0	22:1	24:0	24:1
	%	%	%	%	%	%	%	%	%	%	%	%	%	%
-8	4.59	0.22	3.4	70.77	0	16.71	0	1.35	0	1.14	0.48	0.02	0.39	0.15
-9	4.63	0.23	3.51	69.66	2.01	8.77	7.24	0.97	0	1.18	0.52	0.02	0.3	0.11
-10	4.56	0.19	3.55	70.68	0	16.89	0	1.37	0	1.22	0.54	0.02	0.22	0.03
5538-3-1	4.74	0.21	3.43	67.52	1.29	10.91	7.77	1.03	0.28	1.11	0.5	0.02	0.35	0.14
-2	4.72	0.21	3.24	67.42	1.63	10.37	8.4	0.99	0	1.12	0.49	0.02	0.36	0.15
-3	4.24	0.21	3.52	71.31	0	16.53	0	1.33	0	1.12	0.45	0.02	0.4	0.14
-4	4.64	0.21	3.45	67.92	1.65	9.91	7.97	0.91	0.33	1.14	0.47	0.02	0.37	0.14
-5	4.91	0.25	3.31	67.19	0	19.92	0.01	1.39	0	1.05	0.48	0.02	0.37	0.14
-6	4.67	0.21	3.25	67.07	1.23	11.32	8.35	0.99	0	1.16	0.47	0.02	0.33	0.16
-7	4.53	0.19	2.94	64.8	4.94	8.45	9.95	0.93	0.44	1.13	0.37	0.01	0.27	0.12
-8	4.66	0.22	3.68	67.33	0.71	12	6.99	1.1	0.24	1.18	0.48	0.03	0.36	0.17
-9	4.65	0.24	3.11	67.42	0.64	12.71	6.93	1.16	0.25	1.08	0.45	0.02	0.32	0.17
-10	4.88	0.27	3.33	65.75	0.86	12.89	7.7	1.1	0.24	1.08	0.46	0.01	0.34	0.16
5538-4-1	4.65	0.24	3.8	62.41	0	24.68	0	1.6	0.01	0.99	0.45	0.02	0.33	0.13
-2	5.37	0.31	3	57.98	0.38	18.04	10.5	1.41	0	0.99	0.48	0.02	0.3	0.19
-3	4.61	0.22	3.07	63.62	0.3	16.46	7.67	1.2	0	1.18	0.45	0.02	0.29	0.14

Table 5
Fatty Acid Analysis of Seeds from Ma524 Transgenic *Brassica* Plants

SPL	16:0	16:1	18:0	18:1	6,9 18:2	18:2	18:3ga	18:3	18:4	20:1	22:0	22:1	24:0	24:1
#	%	%	%	%	%	%	%	%	%	%	%	%	%	%
-4	4.39	0.19	2.93	65.97	0	22.36	0	1.45	0	1.17	0.41	0.03	0.32	0.15
-5	5.22	0.29	3.85	62.1	2.35	10.25	11.39	0.93	0.41	1.04	0.6	0.02	0.47	0.17
-6	4.66	0.18	2.85	66.79	0.5	13.03	7.66	0.97	0.22	1.28	0.42	0.02	0.31	0.14
-7	4.85	0.26	3.03	57.43	0.26	28.04	0.01	2.59	0.01	1.13	0.56	0.02	0.4	0.23
-8	5.43	0.28	2.94	54.8	1.84	13.79	15.67	1.36	0.53	1.1	0.55	0.02	0.35	0.19
-9	4.88	0.24	3.32	62.3	0.58	14.86	9.04	1.34	0.29	1.13	0.52	0.02	0.37	0.19
-10	4.53	0.2	2.73	64.2	0.07	24.15	0	1.62	0	1.09	0.39	0.02	0.27	0.17
5538-5-1	4.5	0.15	3.35	66.71	0.88	11.7	8.38	1.04	0.3	1.24	0.49	0.02	0.29	0.17
-2	4.77	0.23	3.06	62.67	0.68	15.2	8.8	1.31	0.28	1.15	0.46	0.02	0.3	0.19
-3	4.59	0.22	3.61	64.35	2.29	9.95	10.57	1.01	0.45	1.21	0.48	0.02	0.26	0.16
-4	4.86	0.26	3.4	67.69	0.65	12.24	6.61	1.09	0.23	1.07	0.45	0.02	0.32	0.14
-5	4.49	0.21	3.3	69.25	0.04	16.51	2.18	1.2	0	1.11	0.44	0.02	0.33	0.16
-6	4.5	0.21	3.47	70.48	0.08	14.9	2.19	1.22	0	1.13	0.49	0.02	0.33	0.16
-7	4.39	0.21	3.44	67.59	2.38	9.24	8.98	0.89	0	1.18	0.44	0.02	0.28	0.14
-8	4.52	0.22	3.17	68.33	0.01	18.91	0.73	1.32	0.01	1.08	0.45	0.02	0.29	0.17
-9	4.68	0.2	3.05	64.03	1.93	11.03	11.41	1.02	0.01	1.15	0.39	0.02	0.21	0.15

Table 5
Fatty Acid Analysis of Seeds from Ma524 Transgenic *Brassica* Plants

SPL	#	16:0	16:1	18:0	18:1	6,9 18:2	18:2	18:3ga	18:3	18:4	20:1	22:0	22:1	24:0	24:1
	%	%	%	%	%	%	%	%	%	%	%	%	%	%	%
	-10	4.57	0.2	3.1	67.21	0.61	12.62	7.68	1.07	0.25	1.14	0.43	0.02	0.25	0.15
5538-8-1	4.95	0.26	3.14	64.04	0	23.38	0	1.54	0	0.99	0.42	0.02	0.38	0.17	
-2	4.91	0.26	3.71	62.33	0	23.97	0	1.77	0	0.95	0.53	0.02	0.42	0.19	
-3	4.73	0.25	4.04	63.83	0	22.36	0.01	1.73	0	1.05	0.55	0.02	0.45	0.16	
-4	5.1	0.35	3.8	60.45	0	24.45	0.01	2.13	0	1.07	0.65	0.03	0.53	0.24	
-5	4.98	0.3	3.91	62.48	0	23.44	0	1.77	0	1.01	0.51	0.01	0.43	0.21	
-6	4.62	0.21	3.99	66.14	0	20.38	0	1.48	0	1.15	0.53	0.02	0.48	0.19	
-7	4.64	0.22	3.55	64.6	0	22.65	0	1.38	0	1.09	0.45	0.02	0.41	0.19	
-8	5.65	0.38	3.18	56.6	0	30.83	0.02	0.02	0	0.98	0.55	0.03	0.39	0.26	
-9	8.53	0.63	6.9	51.76	0	26.01	0	0.01	0	1.41	1.21	0.07	0.96	0.33	
-10	5.52	0.4	3.97	57.92	0	28.95	0	0.02	0	0.95	0.52	0.02	0.41	0.16	
5538-10-1	4.44	0.19	3.5	68.42	0	19.51	0	1.32	0	1.14	0.45	0.02	0.31	0.16	
	-2	4.57	0.21	3.07	66.08	0	21.99	0.01	1.36	0	1.12	0.41	0.02	0.31	0.16
	-3	4.63	0.21	3.48	67.43	0	20.27	0.01	1.32	0	1.12	0.46	0.02	0.21	0.08
	-4	4.69	0.19	3.22	64.62	0	23.16	0	1.35	0	1.08	0.46	0.02	0.33	0.2
	-5	4.58	0.2	3.4	68.75	0	20.17	0.01	0.02	0	1.1	0.45	0.02	0.34	0.17

Table 5
Fatty Acid Analysis of Seeds from Ma524 Transgenic *Brassica* Plants

SPL #	16:0	16:1	18:0	18:1	6,9 18:2	18:2	18:3ga	18:3	18:4	20:1	22:0	22:1	24:0	24:1
#	%	%	%	%	%	%	%	%	%	%	%	%	%	%
-8	4.55	0.21	0	73.55	0.05	14.91	2.76	1.21	0.07	1.24	0.51	0.02	0.19	0
-9	4.58	0.21	3.28	66.19	0	21.55	0	1.35	0	1.12	0.43	0.02	0.33	0.16
-10	4.52	0.2	3.4	68.37	0	19.33	0.01	1.3	0	1.13	0.46	0.02	0.35	0.18

Example 9**Expression of *M. alpina* Δ12 desaturase in *Brassica napus***

The Ma648 cDNA was modified by PCR to introduce cloning sites using the following primers:

5 Ma648PCR-for (SEQ ID NO:29)
5'-CUACUACUACUAGGATCCATGGCACCTCCAACACT
Ma648PCR-rev (SEQ ID NO:30)
5'-CAUCAUCAUCAUGGTACCTCGAGTTACTTCTTGAAAAAGAC

These primers allowed the amplification of the entire coding region and added a BamHI site to the 5' end and KpnI and XhoI sites to the 3' end. The PCR product was subcloned into pAMP1 (GIBCOBRL) using the CloneAmp system (GIBCOBRL) to create pCGN5540 and the Δ12 desaturase sequence was verified by sequencing of both strands.

For seed-specific expression, the Ma648 coding region was cut out of pCGN5540 as a BamHI/XhoI fragment and inserted between the BglII and XhoI sites of the napin expression cassette, pCGN3223, to create pCGN5542. The Asp718 fragment of pCGN5541 containing the napin 5' regulatory region, the Ma648 coding region, and the napin 3' regulatory region was inserted into the Asp718 site of pCGN5138 to create pCGN5542. PCGN5542 was introduced into two varieties of *Brassica napus* via *Agrobacterium* mediated transformation. The commercial canola variety, SP30021, and a low-linolenic line, LP30108 were used.

Mature selfed T2 seeds were collected from 19 independent LP30108 transformation events and a non-transformed control grown in the greenhouse. These seeds are expected to be segregating for the Δ12 desaturase transgene. The fatty acid composition of 20-seed pools was analyzed by GC. The results are shown in Table 6. All transformed lines contained increased levels of 18:2, the product of the Δ12 desaturase. Levels of 18:3 were not significantly increased in these plants. Events # 11 and 16 showed the greatest accumulation

of 18:2 in the pooled seeds. To investigate the segregation of 18:2 levels in the T2 seeds and to identify individual plants to be taken on to subsequent generations, half-seed analysis was done. Seeds were germinated overnight in the dark at 30 degrees on water-soaked filter paper. The outer cotyledon was 5 excised for GC analysis and the rest of the seedling was planted in soil. Results of some of these analyses are shown in Table 7. Individual T2 seeds containing the *M. alpina* Δ12 desaturase accumulated up to 60% 18:2 in the seeds. Sample 97xx1116 #59 is an example of a null segregant. Even in the highest 18:2 accumulators, levels of 18:3 were increased only slightly. These and other 10 individually selected T2 plants were grown in the greenhouse and in the field to produce T3 seed.

Mature selfed T2 seeds were collected from 20 independent SP30021 transformation events and a non-transformed control grown in the greenhouse. These seeds are expected to be segregating for the Δ12 desaturase transgene. 15 The fatty acid composition of 20-seed pools was analyzed by GC. The data are presented in Table 8. All transformed lines contained increased levels of 18:2, the product of the Δ12 desaturase. As in the low-linolenic LP30108 line, levels of 18:3 were not significantly increased. Events # 4 and 12 showed the greatest accumulation of 18:2 in the pooled seeds. To investigate the segregation of 20 18:2 levels in the T2 seeds and to identify individual plants to be taken on to subsequent generations, alf-seed analysis was done. Seeds were germinated overnight in the dark at 30 degrees on water-soaked filter paper. The outer cotyledon was excised for GC analysis and the rest of the seedling was planted in soil. Results of some of these analyses are shown in Table 9. Samples 25 97xx1157 #88 and #18 are examples of null segregants for 5542-SP30021-4 and 5542-SP30021-12 respectively. These and other individually selected T2 plants were grown in the greenhouse and in the field to produce T3 seed

Table 6

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
97XX1098	45	5542-LP30108-16	7.04	0.43	1.12	18.01	66.36	4.76	0.5	0.84	0.3	0.44
97XX1098	22	5542-LP30108-16	5.17	0.29	2.11	22.01	65.18	3.15	0.63	0.75	0.21	0.36
97XX1098	40	5542-LP30108-16	4.99	0.2	2.05	23.91	63.13	3.3	0.73	0.85	0.23	0.49
97XX1098	28	5542-LP30108-16	4.47	0.19	1.75	26.7	62.39	2.46	0.58	0.85	0.2	0.32
97XX1098	2	5542-LP30108-16	4.54	0.21	1.66	26.83	61.89	2.9	0.55	0.82	0.18	0.33
97XX1098	58	5542-LP30108-16	6.05	0.31	1.36	24.11	61.36	3.8	0.72	1.13	0.26	0.58
97XX1098	83	5542-LP30108-16	5.13	0.17	2.03	27.05	60.93	2.62	0.7	0.71	0.14	0.4
97XX1098	34	5542-LP30108-16	4.12	0.19	1.44	29.35	60.54	2.53	0.43	0.89	0.17	0.25
97XX1116	37	5542-LP30108-11	4	0.14	2.43	23.29	63.99	2.6	0.58	0.69	0.71	1.11
97XX1116	88	5542-LP30108-11	3.8	0.18	2.04	23.59	63.93	2.95	0.54	0.81	0.99	0.82
97XX1116	36	5542-LP30108-11	4.15	0.2	1.51	25.94	62.14	2.74	0.47	0.87	0.79	0.81
97XX1116	31	5542-LP30108-11	6.29	0.35	1.04	24.14	60.91	4.02	0.55	0.91	0.75	0.72
97XX1116	10	5542-LP30108-11	6.97	0.4	3.36	18.9	60.66	4.68	1.2	0.7	0.53	1.71
97XX1116	32	5542-LP30108-11	3.96	0.16	2.61	26.73	60.54	3.38	0.66	0.87	0.2	0.62
97XX1116	55	5542-LP30108-11	4.26	0.22	0.98	28.57	59.94	3.24	0.4	0.68	0.71	0.75
97XX1116	12	5542-LP30108-11	4.17	0.23	1.42	28.61	59.52	3.26	0.51	0.95	0.29	0.67

Table 6

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
97XX1116	86	5542-LP30108-11	4.23	0.3	1.09	28.34	59.2	3.95	0.48	0.91	0.55	0.71
97XX1116	61	5542-LP30108-11	4.13	0.16	1.92	30.18	58.67	2.65	0.56	0.88	0.25	0.41
97XX1116	60	5542-LP30108-11	4.42	0.26	1.61	28.77	58.6	3.26	0.53	0.85	0.68	0.75
97XX1116	91	5542-LP30108-11	7.82	0.67	2.37	17.97	58.43	4.85	0.94	0.86	3.87	1.71
97xx1116	59	5542-LP30108-11	3.56	0.2	1.6	65.5	23.03	2.23	0.52	1.54	0.49	0.69

Table 7

	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
	%	%	%	%	%	%	%	%	%	%
5542-LP30108-1	4.6	0.15	1.93	50.44	38.54	2.06	0.65	1.11	0.09	0.37
5542-LP30108-2	4.63	0.17	1.78	41.11	47.53	2.46	0.62	1.02	0.14	0.38
5542-LP30108-3	4.96	0.18	2.07	48.16	40.01	2.17	0.73	1.13	0.1	0.39
5542-LP30108-4	4.36	0.15	1.94	46.51	42.57	1.95	0.64	1.06	0.11	0.35
5542-LP30108-5	4.45	0.14	2.19	49.54	39.13	2.14	0.72	1.14	0.11	0.38
5542-LP30108-6	4.97	0.16	1.86	49.23	39.2	2.17	0.7	1.12	0.11	0.41
5542-LP30108-7	4.46	0.13	2.72	39.6	48.65	2.02	0.81	0.96	0.13	0.4
5542-LP30108-8	4.63	0.18	1.78	47.86	41	2.31	0.62	1.09	0.11	0.36
5542-LP30108-9	4.64	0.16	1.75	42.5	46.57	2.2	0.61	1	0.13	0.35
5542-LP30108-10	4.46	0.15	2.37	43.61	45.29	1.77	0.71	1.02	0.12	0.36
5542-LP30108-11	4.58	0.25	1.88	37.08	50.95	2.94	0.64	0.96	0.16	0.42
5542-LP30108-12	4.46	0.18	1.69	43.62	45.36	2.44	0.59	1.09	0.14	0.34
5542-LP30108-13	4.45	0.15	2.33	51	37.71	1.91	0.75	1.12	0.09	0.4
5542-LP30108-14	4.3	0.16	2.04	45.93	42.78	2.46	0.66	1.07	0.14	0.37
5542-LP30108-15	4.18	0.16	2.17	43.79	45.2	2.14	0.68	1.04	0.15	0.36
5542-LP30108-16	5.04	0.18	1.89	32.32	55.78	2.68	0.63	0.84	0.2	0.36

Table 7

	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
	%	%	%	%	%	%	%	%	%	%
5542-LP30108-18	4.2	0.14	2.23	50.63	38.51	1.79	0.72	1.15	0.1	0.37
5542-LP30108-19	4.63	0.18	1.81	52.51	36.26	2.12	0.68	1.19	0.1	0.4
5542-LP30108-20	4.77	0.15	2.78	39.76	48.06	2.25	0.75	0.91	0.13	0.36
LP30108 control	4.31	0.22	2.05	66.15	22.59	1.87	0.77	1.3	0.07	0.44

Table 8

STRAIN ID	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
5542-SP30021-1	4.37	0.17	2.17	40.26	39.43	11.06	0.74	1.14	0.14	0.42
5542-SP30021-2	4.33	0.18	1.51	43.07	36.03	12.57	0.57	1.21	0.14	0.33
5542-SP30021-3	5.2	0.22	3.1	43.7	37.04	8.03	0.92	1.06	0.13	0.48
5542-SP30021-4	4.37	0.15	1.94	34.26	45.12	12.04	0.6	0.96	0.17	0.3
5542-SP30021-5	4.15	0.17	1.73	48.98	31.13	11.41	0.63	1.26	0.13	0.35
5542-SP30021-6	4.52	0.17	1.92	38.1	42.39	10.53	0.67	1.04	0.18	0.39
5542-SP30021-7	4.58	0.18	1.66	41.87	37.52	11.8	0.62	1.14	0.15	0.36
5542-SP30021-8	4.46	0.17	1.59	42.69	36.93	11.88	0.59	1.14	0.14	0.35
5542-SP30021-9	4.63	0.19	1.69	39.89	39.75	11.48	0.62	1.09	0.15	0.38
5542-SP30021-10	4.74	0.16	1.79	39.19	40.51	11.42	0.63	0.99	0.13	0.34
5542-SP30021-11	4.57	0.16	1.71	38.13	42	11.15	0.62	1.04	0.18	0.36
5542-SP30021-12	4.05	0.16	2.04	35.44	43.47	12.45	0.62	1.07	0.21	0.33
5542-SP30021-13	4.37	0.15	1.79	38.74	41.28	11.36	0.62	1.04	0.16	0.35
5542-SP30021-14	4.32	0.16	1.47	42.32	37.17	12.3	0.54	1.16	0.16	0.32
5542-SP30021-15	4.25	0.18	1.65	44.96	34.28	12.39	0.59	1.13	0.14	0.32

Table 8

STRAIN ID	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
5542-SP30021-16	4.53	0.17	1.91	42.13	38.32	10.51	0.67	1.12	0.14	0.38
5542-SP30021-17	4.16	0.19	1.7	50.65	29.3	11.4	0.61	1.29	0.11	0.36
5542-SP30021-18	4.24	0.17	1.68	44.47	35.46	11.52	0.6	1.19	0.14	0.34
5542-SP30021-19	4.1	0.18	1.8	46.67	33.87	10.86	0.63	1.24	0.13	0.37
5542-SP30021-20	4.3	0.17	1.64	39.6	40.39	11.53	0.57	1.12	0.16	0.32
SP30021	4.38	0.21	1.47	56.51	22.59	12.04	0.62	1.45	0.11	0.39

Table 9

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
97XX1156	96	5542-SP30021-4	3.71	0.13	1.36	29.29	51.74	11.57	0.41	0.85	0.18	0.46
97XX1156	50	5542-SP30021-4	2.95	0.11	1.33	28.78	50.97	13.83	0.3	0.99	0.28	0.32
97XX1158	10	5542-SP30021-4	4.05	0.16	2.47	31.18	50.88	8.77	0.67	0.89	0.22	0.33
97XX1158	32	5542-SP30021-4	3.56	0.15	1.44	30.73	50.1	11.86	0.47	0.91	0.21	0.22
97XX1158	56	5542-SP30021-4	4.44	0.19	3.09	30.64	49.71	9.39	0.83	0.79	0.2	0.4
97XX1157	80	5542-SP30021-4	4.05	0.18	1.32	27.41	49.59	14.81	0.53	1.19	0.29	0.4
97XX1158	39	5542-SP30021-4	4.04	0.15	2.98	28.62	49.52	12.28	0.69	0.86	0.31	0.27
97XX1156	17	5542-SP30021-4	3.65	0.15	2.43	29.38	49.42	12.3	0.52	0.92	0.67	0.35
97XX1156	60	5542-SP30021-4	3.75	0.17	1.7	30.03	49.13	12.87	0.51	1.01	0.27	0.35
97XX1157	83	5542-SP30021-4	4.15	0.2	1.77	29.72	49.08	12.22	0.66	1.21	0.16	0.52
97XX1157	86	5542-SP30021-4	3.6	0.14	1.12	27.65	49.01	16.05	0.48	1.21	0.33	0.08
97XX1158	77	5542-SP30021-4	4.14	0.17	1.58	31.98	48.82	10.72	0.65	1	0.28	0.44
97XX1157	88	5542-SP30021-4	3.36	0.15	1.22	56.42	21.63	13.78	0.58	1.85	0.06	0.65

Table 9

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0
97XX1157	39	5542-SP30021-12	2.84	0.04	1.84	29.6	53.16	9.52	0.57	1.32	0.35	0.48
97XX1157	55	5542-SP30021-12	3.28	0.1	2.18	30.36	52.27	9.26	0.63	1.15	0.22	0.41
97XX1157	10	5542-SP30021-12	3.5	0.06	1.51	29.78	50.98	11.13	0.64	1.45	0.4	0.26
97XX1157	41	5542-SP30021-12	3.31	0.08	1.64	30.18	50.51	11.59	0.57	1.27	0.24	0.41
97XX1157	35	5542-SP30021-12	3.31	0.09	1.57	30.36	50.1	12.17	0.5	1.15	0.23	0.35
97XX1157	1	5542-SP30021-12	3.45	0.11	2.88	32.11	49.45	8.69	0.82	1.22	0.27	0.63
97XX1157	16	5542-SP30021-12	2.91	0.09	1.52	29.35	48.88	14.26	0.58	1.39	0.15	0.3
97XX1157	50	5542-SP30021-12	3.29	0.09	2.13	33.23	48.78	9.87	0.67	1.06	0.18	0.47
97XX1157	25	5542-SP30021-12	2.83	0.05	1.4	33.22	48.52	11.22	0.5	1.33	0.26	0.42
97XX1157	57	5542-SP30021-12	2.94	0.13	1.46	32.85	47.58	12.21	0.57	1.31	0.27	0.47
97XX1157	56	5542-SP30021-12	3.01	0.07	1.63	31.53	47	14.02	0.59	1.31	0.28	0.23
97XX1157	6	5542-SP30021-12	3.9	0.13	1.5	32.43	46.98	12.45	0.52	1.11	0.21	0.49
97XX1157	18	5542-SP30021-12	3.88	0.16	1.73	57.94	22.33	10.51	0.74	1.68	0.11	0.64

Example 10Simultaneous expression of *M. alpina* Δ6 and Δ12 desaturases in *Brassica napus*

5 In order to express the *M. alpina* Δ6 and Δ12 desaturases from the same T-DNA, the following construct for seed-specific expression was made.

10 The NotI fragment of pCGN5536 containing the napin 5' regulatory region, the Ma524 coding region, and the napin 3' regulatory region was inserted into the NotI site of pCGN5542 to create pCGN5544. The expression modules were oriented in such a way that the direction of transcription from Ma524 and Ma648 and the nptII marker is the same.

15 PCGN5544 was introduced into *Brassica napus* cv.LP30108 via *Agrobacterium* mediated transformation. Mature selfed T2 seeds were collected from 16 independent LP30108 transformation events and a non-transformed control that were grown in the greenhouse. These seeds are expected to be segregating for the Δ6+ Δ12 desaturase transgene. The fatty acid composition of 20-seed pools was analyzed by GC. The results are presented in Table 10. All but one of the lines (5544-LP30108-3) shows an altered oil composition as compared to the controls. GLA was produced in all but three of the lines (-3, -4, -11); two of the three without GLA (-4, -11) showed increased 18:2 indicative of expression of the Δ12 desaturase. As a group, the levels of GLA observed in plants containing the double Δ6 + Δ12 construct (pCGN5544) were higher than those of plants containing pCGN5538 (Δ6 alone). In addition, levels of the Δ^{6,9} 18:2 are much reduced in the plants containing the Δ12 + Δ6 as compared to Δ6 alone. Thus, the combination of Δ6 and Δ12 desaturases on one T-DNA leads to the accumulation of more GLA and fewer side products than expression of Δ6 desaturase alone. To investigate the segregation of GLA levels in the T2 seeds and to identify individual plants to be taken on to subsequent generations, half-seed analysis was done. Seeds were germinated overnight in the dark at 30 degrees on water-soaked filter paper. The outer cotyledon was excised for GC analysis and the rest of the seedling was planted in soil. Results of some of

these analyses are shown in Table 11. As expected for the T2 population, levels of GLA and 18:2 are segregating in the individual seeds. GLA content of up to 60% of total fatty acids was observed in individual seeds. Individual events were selected to be grown in the greenhouse and field for production of T3 seed.

Transgenic plants including *Brassica*, soybean, safflower, corn flax and sunflower expressing the constructs of this invention can be a good source of GLA.

Typical sources of GLA such as borage produce at most 25% GLA. In contrast the plants in Table 10 contain up to 30% GLA. Furthermore, the individual seeds shown in Table 11 contain up to 60% GLA.

Table 10

	16:0	16:1	18:0	18:1	18:2	18:3	18:3	18:4	20:0	20:1	22:0
	%	%	%	%	%	%	%	%	%	%	%
5544-LP30108-1	4.54	0.17	1.91	49.96	0	30.98	7.97	1.85	0.11	0.68	1.17
5544-LP30108-2	4.69	0.19	2.15	38.49	0	33.94	16.21	1.73	0.25	0.72	0.96
5544-LP30108-3	4.26	0.2	1.97	66.68	0	22.13	0.08	1.96	0.01	0.73	1.33
5544-LP30108-4	4.59	0.24	1.76	44.21	0	44.54	0.02	2.19	0.01	0.62	1.08
5544-LP30108-5	4.5	0.18	2.28	47.57	0	26.41	14.42	1.71	0.22	0.78	1.1
5544-LP30108-6	4.51	0.16	2.12	31.95	0.01	26.94	29.8	1.41	0.5	0.81	1.02
5544-LP30108-7	4.84	0.21	1.68	38.24	0	32.27	18.21	1.87	0.33	0.66	1.04
5544-LP30108-10	5	0.28	1.86	41.17	0	46.54	0.36	2.58	0.02	0.6	0.91
5544-LP30108-11	4.57	0.2	1.74	47.29	0	41.49	0.03	2.22	0.01	0.64	1.17
5544-LP30108-12	4.87	0.18	2.65	34.53	0	30.37	23.12	1.46	0.36	0.83	0.95
5544-LP30108-13	4.41	0.16	2.32	40.82	0.11	26.8	21.05	1.53	0.37	0.77	1.06
5544-LP30108-14	4.38	0.2	2.21	29.91	0.16	28.01	30.62	1.46	0.59	0.76	0.97
5544-LP30108-15	4.79	0.22	2.23	23.42	0.02	28.73	35.68	1.51	0.77	0.87	0.89
5544-LP30108-16	4.54	0.18	1.78	40.81	0	35.24	12.83	1.95	0.27	0.68	1.02
5544-LP30108-17	4.63	0.18	2.28	46.96	0	31.06	10.6	1.7	0.14	0.76	1.06
5544-LP30108-20	4.87	0.29	1.44	31.81	0.15	23.51	32.85	1.64	0.69	0.89	0.96

Table 10

	16:0	16:1	18:0	18:1	18:2	18:2	18:3	18:3	18:4	20:0	20:1	22:0
	%	%	%	%	%	%	%	%	%	%	%	%
Δ6,9					Δ9,12	Δ6,9,12	Δ6,9,12	Δ9,12, 15				
LP30108 control	3.89	0.25	1.19	67.73	0	22.46	0.1	1.97	0	0.54	1.32	0.44

Table 11

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9,	18:3_Δ9,12,	18:4	20:0	20:1
									<u>12</u>	<u>15</u>			
97XX1333	64	5544-LP30108-20	6.53	0.15	0.98	23.33	0.01	21.1	43.3	1.34	0.84	0.52	0.97
97XX1333	65	5544-LP30108-20	6.9	0.29	1.17	8.89	0.03	15.07	60.5	1.12	2.23	0.98	0.86
97XX1333	66	5544-LP30108-20	8.15	0.2	3.6	16.87	0.11	16.05	48.23	1.1	1.18	1.71	0.66
97XX1333	67	5544-LP30108-20	8.85	0.35	1.2	14.49	0.01	25.66	43.98	1.8	1.03	0.65	0.76
97XX1333	68	5544-LP30108-20	6.05	0.16	1.27	17.85	0.16	16.13	53.16	1.14	1.25	0.71	0.85
97XX1333	69	5544-LP30108-20	7.16	0.21	1.33	11.51	0.09	17.42	56.13	1.41	1.58	0.93	0.68
97XX1333	70	5544-LP30108-20	3.46	0.04	1.76	18.38	0.03	22.55	48.55	1.22	1.04	0.83	0.95
97XX1333	71	5544-LP30108-20	3.71	0.05	1.74	16.11	0.01	26.93	45.79	1.47	1.02	0.89	1
97XX1333	72	5544-LP30108-20	3.5	0.04	1.76	23.74	0.02	35.38	30.82	1.87	0.58	0.65	0.89
97XX1333	73	5544-LP30108-20	4.67	0.11	1.87	17.98	0.04	22.47	47.89	1.17	0.89	0.93	0.88
97XX1333	74	5544-LP30108-20	4.52	0.09	1.86	13.77	0.03	20.9	52.96	1.31	1.19	1.03	0.88
97XX1333	75	5544-LP30108-20	5.26	0.13	1.64	16.46	0.05	21.75	49.42	1.25	1.08	0.83	0.86
97XX1333	76	5544-LP30108-20	7.61	0.21	1.44	12.49	0.33	17	55.31	1.18	1.59	0.88	0.74
97XX1333	77	5544-LP30108-20	6.42	0.15	1.51	10.79	0.09	15.96	58.77	1.12	1.53	0.98	0.85
97XX1333	78	5544-LP30108-20	4.59	0.16	0.93	12.1	0.08	15.94	60.15	1.12	1.69	0.74	0.88
97XX1333	79	5544-LP30108-20	5.24	0.09	1.94	14.08	0.21	19.79	53.58	1.05	1.03	0.96	0.84

Table 11

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9 12	18:3_Δ9,12, 15	18:4	20:0	20:1
97XX1333	80	5544-LP30108-20	4.38	0.08	1.66	22.25	0	30.79	35.49	2.16	0.72	0.66	0.84
97XX1333	81	5544-LP30108-20	4.05	0.05	1.44	24.16	0.04	24.86	40.89	1.42	0.79	0.63	0.84
97XX1333	82	5544-LP30108-20	3.29	0.05	1.9	19.66	0	23.83	46.48	1.27	0.87	0.78	0.81
97XX1333	83	5544-LP30108-20	4.82	0.08	1.99	17.27	0.1	20.69	49.73	1.22	1.06	0.98	0.82
97XX1333	84	5544-LP30108-20	5.33	0.1	1.77	13.6	0.03	21.44	51.74	1.52	1.21	0.98	0.93
97XX1333	85	5544-LP30108-20	3.3	0.05	1.2	68.23	0	22.09	0.01	2.27	0	0.57	1.57
97XX1333	86	5544-LP30108-20	3.23	0.05	1.54	28.15	0.01	36.4	25.91	1.99	0.43	0.59	0.97
97XX1333	87	5544-LP30108-20	4.38	0.1	1.16	60.94	2.85	8.35	17.61	1.26	0.69	0.54	1.39
97XX1333	88	5544-LP30108-20	4.4	0.09	1.34	38.42	0.02	34.74	16.61	2.12	0.32	0.53	0.82
97XX1278	16	5544-LP30108-15	3.62	0.11	1.22	27.23	0	30.9	32.87	1.41	0.48	0.46	0.97
97XX1278	17	5544-LP30108-15	3.68	0.13	1.26	45.29	0	44.79	0.72	1.77	0.01	0.43	1.24
97XX1278	18	5544-LP30108-15	4.08	0.15	1.49	22.34	0	28.37	39.37	1.22	0.64	0.55	0.88
97XX1278	19	5544-LP30108-15	3.51	0.1	1.01	35.44	0	44.12	11.7	1.72	0.15	0.36	1.14
97XX1278	20	5544-LP30108-15	3.66	0.12	1.21	27.44	0	30.2	32.37	1.49	0.53	0.49	1.15
97XX1278	21	5544-LP30108-15	3.58	0.11	1.51	29.81	0	30.72	30.65	1.16	0.4	0.5	0.96
97XX1278	23	5544-LP30108-15	3.69	0.11	1.42	30.05	0	32.28	27.41	1.65	0.38	0.54	1.19
97XX1278	24	5544-LP30108-15	3.56	0.11	1.31	30.25	0	28.64	31.46	1.43	0.48	0.48	1.11

Table 11

CYCLE ID	SPL NO	STRAIN ID	16:0	16:1	18:0	18:1	18:2_A6,9	18:2_A9,12	18:3_A6,9	18:3_A9,12,	18:4	20:0	20:1
97XX1278	25	5544-LP30108-15	4.41	0.22	2.08	15.05	0	23.77	49.51	1.18	0.96	0.87	0.85
97XX1278	26	5544-LP30108-15	3.75	0.14	1.59	23.55	0	27.91	38.8	1.39	0.61	0.59	0.97
97XX1278	27	5544-LP30108-15	3.67	0.11	1.9	26.07	0	31.1	33.16	1.08	0.49	0.65	0.97
97XX1278	28	5544-LP30108-15	3.82	0.11	1.54	21.27	0	29.07	39.69	1.47	0.7	0.58	0.86
97XX1278	29	5544-LP30108-15	3.65	0.14	1.27	45.84	0	43.38	1	2.33	0.02	0.42	1.27
97XX1278	30	5544-LP30108-15	3.59	0.12	1.19	30.41	0	30.68	30.37	1.24	0.4	0.37	0.99
97XX1278	31	5544-LP30108-15	3.74	0.12	1.26	38.98	0	50.53	0.98	2.12	0.02	0.39	1.14
97XX1278	32	5544-LP30108-15	3.86	0.11	1.46	26.38	0	28.9	35.41	1.01	0.5	0.54	0.97

Example 11**Simultaneous expression of *M. alpina* Δ5 and Δ6 desaturases in *Brassica napus***

5 In order to produce arachidonic acid (ARA) in transgenic canola oil both Δ5 and Δ6 desaturase activities need to be introduced. In order to facilitate downstream characterization and breeding, it may be advantageous to have both activities encoded by a single T-DNA. The following example illustrates the simultaneous expression of Δ5 and Δ6 desaturases.

10 The Asp718 fragment of pCGN5528 containing the napin 5' regulatory region, the Ma29 coding region, and the napin 3' regulatory region was inserted into the Asp718 site of pCGN5138 to create pCGN5545. The NotI fragment of pCGN5536 containing the napin 5' regulatory region, the Ma524 coding region, and the napin 3' regulatory region was inserted into the NotI site of pCGN5545
15 to create pCGN5546. The expression modules were oriented in such a way that the direction of transcription from Ma524 and Ma29 and the nptII marker is the same.

20 pCGN5546 was introduced into *Brassica napus* cv.LP30108 via *Agrobacterium* mediated transformation. Mature selfed T2 seeds were collected from 30 independent LP30108 transformation events that were grown in the greenhouse. The fatty acid composition of 20-seed pools was analyzed by GC. The results are shown in Table 12. All the lines show expression of both desaturases as evidenced by the presence of Δ^{5,9} 18:2 (as seen in pCGN5531 plants) and Δ^{6,9} 18:2 and GLA (as seen in pCGN5538 plants)

25 .

Table 12

fatty acid analysis of 20-seed pools of mature T2 seeds from 5546-LP30108 events

STRAIN ID	16:0	16:1	18:0	18:1	18:2_Δ5,9	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9, 12	18:3_Δ9,12, 15	18:4	20:0	20:1
5546-LP30108-1	4.88	0.33	2.28	57.2	4.68	6.08	7.36	12.29	1.38	0.85	0.84	1.22
5546-LP30108-2	4.01	0.14	2.22	66.04	2.73	1.33	12.6	6.45	1.41	0.32	0.75	1.2
5546-LP30108-3	4.29	0.15	2.55	68.89	0.44	0.58	16.97	1.66	1.6	0.11	0.88	1.22
5546-LP30108-4	4.24	0.14	2.6	70.48	0.73	0.52	14.28	2.61	1.42	0.14	0.96	1.26
5546-LP30108-5	3.52	0.15	2.01	60.3	1.72	0.95	16.92	9.88	1.66	0.39	0.68	1.26
5546-LP30108-6	4.05	0.17	2.24	61.29	1.98	0.4	18.87	6.28	2	0.34	0.7	1.24
5546-LP30108-7	4.74	0.21	2.49	64.5	2.25	1.18	10.03	9.73	1.35	0.52	0.97	1.28
5546-LP30108-8	4.24	0.14	2.82	63.92	1.9	1.5	11.67	9.29	1.44	0.43	0.89	1.19
5546-LP30108-9	3.8	0.13	2.15	65.75	2.3	0.16	14.92	6.32	1.57	0.24	0.75	1.35
5546-LP30108-10	4.28	0.17	1.55	58.8	1.1	0.12	22.95	5.97	2.24	0.22	0.6	1.35
5546-LP30108-11	4.25	0.15	1.82	63.68	1.01	0.22	19.42	4.96	1.81	0.2	0.67	1.23
5546-LP30108-12	3.95	0.14	2.36	66.9	1.12	0.01	19.42	1.59	1.77	0.04	0.8	1.21
5546-LP30108-13	4.18	0.16	2.17	66.91	1.36	0.02	18.84	1.99	1.74	0.05	0.77	1.15
5546-LP30108-14	4.74	0.26	1.82	65.29	1.25	0.27	16.77	5.3	1.59	0.25	0.71	1.32
5546-LP30108-15	4.3	0.23	2.54	65.65	1.67	0.59	13.15	7.22	1.54	0.36	0.88	1.3
5546-LP30108-16	4.05	0.17	2.75	64.13	2.56	2.8	9.56	9.31	1.34	0.53	0.92	1.28

Table 12

fatty acid analysis of 20-seed pools of mature T2 seeds from 5546-LP30108 events

STRAIN ID	16:0	16:1	18:0	18:1	18:2 Δ 5,9	18:2 Δ 6,9	18:2 Δ 9,12	18:3 Δ 6,9, 12	18:3 Δ 9,12, 15	18:4	20:0	20:1
5546-LP30108-17	4.06	0.13	2.85	65.76	2.09	1.92	9.65	9.1	1.23	0.45	0.92	1.22
5546-LP30108-18	4.16	0.25	2.14	60.68	1.43	0.02	24.02	2.62	2.11	0.09	0.69	1.26
5546-LP30108-19	5.77	0.37	2.15	56.11	1.6	0.33	19.34	9.16	2.37	0.46	0.73	1.05
5546-LP30108-20	5.03	0.36	2.34	61.05	1.55	0.35	17.21	6.96	2.24	0.39	0.77	1.22
5546-LP30108-21	4.52	0.3	2.71	62.14	1.33	0.23	17.62	6.44	1.88	0.28	0.88	1.15
5546-LP30108-22	5.91	0.44	2.15	60.12	1.41	0.36	17.04	7.75	1.97	0.36	0.78	1.07
5546-LP30108-23	4.28	0.22	2.44	66.19	0.93	0.11	17.03	4.37	1.67	0.17	0.82	1.25
5546-LP30108-24	4.92	0.33	2.68	62.6	1.32	0.36	16.89	5.82	2.05	0.3	0.95	1.19
5546-LP30108-25	5.42	0.72	3.15	47.47	2.66	4.21	13.51	16.31	2.14	0.99	1.18	1.37
5546-LP30108-26	3.85	0.22	2.78	65.02	1.05	0.05	18.35	4.36	1.67	0.12	0.82	1.18
5546-LP30108-27	3.86	0.15	2.76	65.17	1.11	0.78	16.24	5.21	1.53	0.25	0.93	1.3
5546-LP30108-28	5.29	0.42	1.81	49.12	1.07	0.09	30.52	5.21	3.57	0.44	0.67	1.23
5546-LP30108-29	4.4	0.2	2.38	65.95	1.05	0.28	16.31	4.85	1.64	0.19	0.85	1.26
5546-LP30108-30	3.99	0.19	2.55	67.47	0.83	0.11	17.02	3.18	1.68	0.13	0.83	1.23

Example 12Simultaneous expression of *M. alpina* Δ5, Δ6 and Δ12 desaturases in *Brassica napus*

5 In order to achieve optimal production of ARA in transgenic canola oil both the Δ6 and Δ12 desaturase activities may need to be present in addition to the Δ5 activity. In order to facilitate downstream characterization and breeding, it may be advantageous to have all of these activities encoded by a single T-DNA. The following example illustrates the simultaneous expression of Δ5, Δ6 and Δ12 desaturases.

10 The HindIII fragment of pCGN5528 containing the napin 5' regulatory region, the Ma29 coding region, and the napin 3' regulatory region was inserted into the HindIII site of pCGN5544 to create pCGN5547. The expression modules were oriented in such a way that the direction of transcription from

15 Ma29, Ma524, Ma648 and the nptII marker is the same.

PCGN5547 was introduced into *Brassica napus* cv.LP30108 via *Agrobacterium* mediated transformation. Mature selfed T2 seeds were collected from 30 independent LP30108 transformation events that were grown in the greenhouse. The fatty acid composition of 20-seed pools was analyzed by GC.

20 The results are shown in Table 13. Twenty-seven of the lines show significant accumulation of GLA and in general the levels of GLA observed are higher than those seen in the 5546 plants that did not contain the Δ12 desaturase. The Δ12 desaturase appears to be active in most lines as evidenced by the lack of detectable Δ6,9 18:2 and elevated 18:2 levels in most plants. Small amounts of

25 Δ5,9 18:2 are seen in the 5547 plants, although the levels are generally less than those observed in the 5546 plants. This may be due to the presence of the Δ12 desaturase which efficiently converts the 18:1 to 18:2 before it can be desaturated at the Δ5 position.

Table 13

fatty acid analysis of 20-seed pools of mature T2 seeds from 5547-LP30108 events

STRAIN ID	12:0	16:0	16:1	18:0	18:1	18:2_Δ5, 9	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9, 12	18:3_Δ9,12, 15	18:4	20:0	20:1	22:1	22:2
5547-LP30108-1	0.0	5.38	0.3	2.23	64.12	0.01	0	22.67	0.44	2.17	0.07	0.82	1.11	0.03	0
5547-LP30108-2	0.1	4.45	0.13	2.29	51.57	0.16	0	33.85	3.18	1.74	0.03	0.78	1.02	0.03	0.02
5547-LP30108-3	0.0	4.18	0.12	2.03	59.61	0.03	0	29.44	0.44	1.64	0	0.75	1.15	0.03	0.01
5547-LP30108-4	0.0	4.35	0.15	2.29	50.59	0.12	0.01	37.31	0.85	1.86	0.02	0.78	1.02	0.02	0.01
5547-LP30108-5	0.0	4.59	0.14	1.83	49	0.25	0.01	31.65	8.16	1.86	0.13	0.68	1.04	0.02	0
5547-LP30108-6	0.0	4.11	0.15	2.53	44.3	0.13	0	28.12	15.89	1.94	0.28	0.82	1.13	0	0
5547-LP30108-7	0.0	4.27	0.15	2.55	39.18	0.12	0.02	27	21.72	1.87	0.45	0.89	1.08	0	0
5547-LP30108-8	0.0	4.3	0.14	2.92	42.83	0.26	0	30.81	14.51	1.49	0.22	0.89	1.06	0	0
5547-LP30108-9	0.0	4.46	0.17	3.13	44.51	0	0	30.12	12.87	1.76	0.22	0.98	1.12	0.01	0
5547-LP30108-10	0.0	4.28	0.11	2.62	41.44	0.28	0	30.89	16.28	1.45	0.21	0.82	1.06	0	0
5547-LP30108-11	0.0	4.47	0.17	2.43	26.96	0.48	0	34.44	25.01	2.14	0.63	0.84	0.99	0	0
5547-LP30108-12	0.0	4.36	0.16	2.68	42.2	0.17	0	29.78	15.93	1.83	0.27	0.88	1.06	0	0
5547-LP30108-13	0.0	4.87	0.19	2.81	21.7	0.53	0	32.83	30.54	2.04	0.8	1	0.89	0.02	0.01
5547-LP30108-14	0.0	4.61	0.25	2.6	54	0	0	32.98	0.5	2.46	0.03	0.86	1.14	0	0
5547-LP30108-15	0.0	4.07	0.14	2.98	37.09	0.14	0.01	29.01	21.55	1.66	0.38	1.06	1.11	0	0

Table 13

fatty acid analysis of 20-seed pools of mature T2 seeds from 5547-LP30108 events

STRAIN ID	12:0	16:0	16:1	18:0	18:1	18:2 _{Δ5,9} g	18:2 _{Δ6,9}	18:2 _{Δ9,12}	18:3 _{Δ6,9,12} 15	18:3 _{Δ9,12,}	18:4	20:0	20:1	22:1	22:2
5547-LP30108-16	0.0	3.63	0.13	2.12	64.69	0	0	24.21	0.15	2.04	0	0.82	1.56	0.02	0
5547-LP30108-17	0.0	3.85	0.18	2.22	67.22	0.01	0	21.25	0	2.27	0	0.83	1.53	0	0
5547-LP30108-18	0.0	5.46	0.19	2.87	41.83	0.1	0.04	22.76	21.45	1.72	0.48	1.06	1.23	0	0
5547-LP30108-19	0.0	4.33	0.12	2.73	50.31	0.07	0	24.77	12.72	1.62	0.21	1.04	1.29	0	0.01
5547-LP30108-20	0.0	4.22	0.12	2.91	46.33	0.25	0	26.87	14.65	1.61	0.22	0.98	1.18	0	0
5547-LP30108-21	0.0	4.38	0.17	2.37	55.37	0	0	32.59	0.53	1.85	0.03	0.83	1.23	0	0
5547-LP30108-22	0.0	5.5	0.18	2.71	41.93	0.1	0.19	24.19	20.14	1.76	0.45	0.94	1.21	0	0
5547-LP30108-23	0.0	4.03	0.16	2.17	68.44	0	0	20.09	0	2.19	0.02	0.83	1.46	0	0
5547-LP30108-24	0.0	4.19	0.17	2.72	49.31	0	0	30.38	8.64	1.85	0.13	0.86	1.16	0	0
5547-LP30108-25	0.0	4.04	0.17	2.1	70.48	0	0	18.04	0.05	2.09	0	0.86	1.54	0	0
5547-LP30108-26	0.0	4.74	0.22	3.2	26.74	0.33	0	30.05	28.95	2.02	0.78	1.08	0.99	0	0
5547-LP30108-27	0.0	4.29	0.18	2.23	52.49	0	0	28.48	7.36	1.91	0.13	0.87	1.37	0	0
5547-LP30108-28	0.0	4.36	0.17	3	44.35	0.2	0	29.59	13.39	1.91	0.23	0.96	1.17	0	0
5547-LP30108-29	0.0	4.32	0.17	2.94	52.53	0.05	0	33.88	0.91	2.34	0.01	0.97	1.23	0	0
5547-LP30108-30	0.0	4.07	0.14	2.89	45.13	0.01	0	29.06	13.96	1.71	0.2	0.94	1.2	0.01	0

Example 13**Stereospecific Distribution of Δ6-Desaturated Oils**

This experiment was designed to investigate the stereospecific distribution of the Δ6-desaturated oils in seeds expressing pCGN5538 (Ma 524 cDNA). Three seed samples were used:

- 5 1) Non-transformed *B. napus* cv. LP004 seeds (control)
- 2) Segregating T2 seeds of pCGN5538-LP004-19
- 3) Segregating T2 seeds of pCGN5538-LP004-29

The following protocol was used for the analysis:

10 1. **Seed Oil Extraction**

Fifty seeds were placed in a 12 x 32 mm vial and crushed with a glass rod. 1.25 mL hexane was added and the mixture was vortexed. The seeds were extracted overnight on a shaker. The extract was then filtered through a 0.2 micron filter attached to a 1cc syringe. The extract was then dried down under nitrogen. The resulting oil was used for digestion and derivatization of the whole oil sample.

15 2. **Digestion**

A. **Liquid Oil Digestion**

20 The stock lipase (from *Rhizopus arrhizus*, Sigma, L4384) was diluted to approximately 600,000 units/mL with a goal of obtaining 50% digestion of the TAG. The stock lipase is maintained at 4 degrees C and placed on ice. The amount of reagents may be adjusted according to the amount of oil to be digested.

25 The following amounts are based on a 2.0 mg extracted oil sample. In a 12 x 32 mm screw cap vial the following were added: 2.0 mg oil, 200 µL 0.1 M tris HCl pH 7, 40 µL 2.2 w/v% CaCl₂ 2H₂O, and 100 µL 0.05 w/v % bile salts. The material was vortexed and sonicated to disperse the oil. Twenty µL of diluted lipase was added and the mixture was vortexed continuously for 1.0

minute at room temperature. A white precipitate formed. The reaction was stopped with 100 μ L 6M HCl and vortexing. Five hundred μ L CHCl₃:CH₃OH (2:1) was added and the mixture was vortexed and held on ice while reaining digestions were carried out. Samples were vortexed again and centrifuged
5 briefly to sharpen layers. The lower layer containing digest products was removed with a pasteur pipette and placed in a 12 x 32 mm crimp cap vial. The material was then re-extracted with 300 μ L CHCl₃, vortexed, centrifuged, and combined with the lower layers. The digest products were kept on ice as much as possible. HPLC separation is performed as soon as possible after digestion to
10 minimize acyl migration.

B. Solid Fat Digestion

The procedure for liquid oil digestion described above was followed except that 20 μ l 11:0 methyl ester is added to 2.0 mg solid fat.

3. HPLC Separation

15 The digestion products were dried down in chloroform to approximately 200 μ L. Each sample was then transferred into an insert in an 8 x 40 mm shell vial and 30 μ L was injected for HPLC analysis.

20 The high performance liquid chromatographic system was equipped with a Varex ELSD IIA evaporative light scattering detector with tube temperature at 105°C and nitrogen gas flow at 40 mL/min; a Waters 712 Wisp autosampler, three Beckman 114M Solvent Delivery Modules; a Beckman 421A controller, a Rheodyne pneumatically actuated stream splitter; and a Gilson micro fractionator. The chromatography column is a 220 x 4.6 mm, 5 micron normal phase silica cartridge by Brownlee.

25 The three solvents used were:

A= hexane:toluene 1:1

B= toluene: ethyl acetate 3:1

C= 5% formic acid in ethyl acetate

The gradient profile was as follows:

Time (min)	Function	Value	Duration
0 flow	2.0 mL/min		
0 % B	10		
0 % C	2		
2 % C	25		6 min
14.0 % C	2		1 min
15.0	End program		

A chromatographic standard mixture is prepared in hexane:toluene 1:1 containing the following:

- 0.2 mg/mL triglyceride 16:0
- 5 2.0 mg/mL 16:0 Free Fatty Acid
- 0.2 mg/mL di16:0 mixed isomers (1,2-diacylglycerol and 1,3-diacylglycerol)
- 0.2 mg/mL 3-mono acylglycerol 16:0
- 0.2 mg/mL 2-mono acylglycerol 16:0

For each sample, the fraction containing the 2-mag peak is collected automatically by method controlled timed events relays. A time delay is used to synchronize the detector with the collector's emitter. The 2-mag peaks are collected and the fractions are evaporated at room temperature overnight.

The *sn*-2 composition results rely on minimization of acyl migration. Appearance of 1-monoacylglycerol and/or 3-monoacylglycerol peaks in the chromatograph means that acyl migration has occurred.

4. Derivatization

To derivatize the whole oil, 1.0 mg of the extracted whole oil was weighed into a 12 x 32 mm crimp cap vial. One mL toluene was then added. The sample is then vortexed and a 50 μ L aliquot was removed for derivatization. To the dried down 2-mag samples, 50 μ L toluene was added. To both the whole oil and 2-mag fractions 105 uL H₂SO₄/CH₃OH @ 8.76 wt% is added. The cap was tightly capped and the sample is refluxed for 1 hour at 95 degrees C. The sample was allowed to cool and 500 uL 10 w/v % NaCl in

water and 60 uL heptane was added. The organic layer was removed and inserted in a 12 x 32 mm crimp cap vial.

5. GLC Analysis

A Hewlett Packard model 6890 GC equipped with a split/splitless capillary inlet, FID detector, 6890 series autosampler and 3392A Alpha Omega integrator is set up for the capillary column as follows:

A. Supelco Omegawax 250, 30 m length, 0.25 mm id, 0.25 um film thickness

10 injection port: 260 C
detector: 270 C
initial temp: 170 C
initial time: 1.5 min
rate: 30 deg/min
15 final temp: 245 C
final time: 6.5 min
injection vol: 1.5 uL
head pressure: 25 psi
split ratio: 30
20 carrier gas: He
make-up gas: N₂
FID gas: H + air

Percent compositions of fatty acid methyl esters are calculated as mole percents. For carbon chain lengths less than 12, the use of theoretical or empirical response factors in the area percent calculation is desirable.
25

6. Calculations

The mean distribution of each acyl group at each *sn*-1 and *sn*-3 position was calculated.

$$\text{mean } sn\text{-}1 \text{ and } sn\text{-}3 \text{ composition} = (3 \text{ WO comp} - \text{MAG comp}) / 2$$

5 WO = whole oil

MAG= monoacylglycerol

The results of this analysis are presented in Table 14. The GLA and $\Delta^{6,9}$ 18:2 are evenly distributed between the *sn*-2 and *sn*-1, 3 positions. This analysis can not discriminate between fatty acids in the *sn*-1 vs. *sn*-3 positions.

Table 14

	16:0	16:1	18:0	18:1	18:2 Δ6,9	18:2	18:3 Δ6,9,12	8:3	18:4	20:0	20:1
Control											
sn2 composition	1.23	0.15	0.37	64.77	0.00	29.45	0.06	2.01	0.00	0.21	0.57
whole oil composition	4.33	0.20	3.32	69.29	0.18	18.51	0.00	1.35	0.06	0.91	1.17
mean sn1, sn3 composition*	5.88	0.23	4.80	71.55	0.27	13.04	-0.03	1.02	0.09	1.26	1.47
5538-19	sn2 composition	1.65	0.27	4.12	57.21	5.61	14.55	12.45	1.38	0.32	0.43
	whole oil composition	5.44	0.33	4.09	57.51	4.53	10.57	13.16	1.03	0.50	1.07
	mean sn1, sn3 composition*	7.34	0.36	4.08	57.66	3.99	8.58	13.52	0.86	0.59	1.39
5538-29	sn2 composition	1.24	0.27	1.56	56.35	6.35	17.85	12.99	1.60	0.38	0.14
	whole oil composition	4.96	0.32	3.73	54.92	4.99	12.11	13.66	1.10	0.50	0.99
	mean sn1, sn3 composition*	6.82	0.35	4.82	54.21	4.31	9.24	14.00	0.85	0.56	1.42

*calculated from the mag and whole oil composition for each analyte

Example 14Fatty Acid Compositions of Transgenic Plants

$\Delta 5$ and $\Delta 6$ transgenic plants were analyzed for their fatty acid content.

The following protocol was used for oil extraction:

- 5 1. About 400 mg of seed were weighed out in duplicate for each sample.
- 10 2. The seeds were crushed in a motar and pestle. The mortar and pestle was rinsed twice with 3ml (2:1) (v:v) CHCl₃:CH₃OH/MeOH. An additional 6 ml (2:1) was added to the 20ml glass vial (oil extracted in 12ml total 2:1).
- 15 3. Samples were vortexed and placed on an orbital shaker for 2 hours with occasional vortexing.
- 20 4. 5ml of 1M NaCl was added to each sample. Sample was vortexed then spun in centrifuge at 2000rpm for 5 minutes. Lower phase was drawn off using a pasteur pipette.
- 25 5. Upper phase was re-extracted with an additional 5ml. Sample was vortexed then spun in centrifuge at 2000 rpm for 5 minutes. The lower phase was drawn off using a pasteur pipette and added to previous lower phase.
- 30 6. CHCl₃:CH₃OH /MeOH was evaporated under nitrogen using evaporative cooling. Vial containing extracted oil was sealed under nitrogen. Between 120mg- 160mg oil was extracted for each sample.

For GC-MS analysis, fatty acid methyl esters were dissolved in an appropriate volume of hexane and analyzed using a Hewlett-Packard 5890 Series II Plus gas chromatograph (Hewlett Packard, Palo Alto, CA) equipped with a 30 m x 0.32 mm i.d. Omegawax 320 fused silica capillary column (Supelco, Bellefonte, PA) and a Hewlett-Packard 5972 Series mass selective detector. Mass spectra were intrepreted by comparison to the mass spectra in

NIST/EPA/NIH Chemical Structure Database using a MS Chem Station (#G1036A) (Hewlett Packard).

Transgenic line 5531-6 was analyzed in duplicate (A, B) and compared to control line LP004-6. The fatty acid profile results are shown in Table 15.

5 Transgenic line 5538-19 was analyzed in duplicate (A, B) and compared to control line LP004-6. The fatty acid profile results are shown in Table 16.

Table 15
Fatty Acid Profile

	CONTROL	CONTROL	TRANSGENIC	TRANSGENIC
	LP004-6A	LP004-6B	5531-6A	5531-6B
	LRL-2043	LRL-2044	LRL-2042	LRL-2045
	001f0102.d	001f0103.d	001f0101.d	001f0104.d
C12:0				
C13:0				
C14:0		0.053		0.061
C14:1				
C15:0 isomer				
C15:0				
C16:0	4.107	4.034	4.257	4.224
C16:1	0.181	0.173	0.200	0.199
C16:2	0.061	0.065	0.081	0.060
C17:0				
C16:3	0.244	0.246	0.155	0.151
C16:4				
C18:0	2.608	2.714	3.368	3.417
C18:1w9	65.489	66.454	59.529	59.073
C18:1w7	2.297	2.185	2.388	2.393
C18:2 5,9			6.144	6.269
C18:2w6	19.828	18.667	18.872	19.059
C18:3 5,9,12			0.469	0.496
C18:3w6		0.060		
C18:3w3	1.587	1.578	1.428	1.418
C18:4w6				
C18:4w3				
C20:0	0.962	0.998	1.009	1.022
C20:1w11	1.336	1.335	1.058	1.065
C20:1w9				
C20:1w7			0.076	0.080
C20:2w6	0.073	0.073		0.052
C20:3w6				

Table 15
Fatty Acid Profile

	CONTROL	CONTROL	TRANSGENIC	TRANSGENIC
	LP004-6A	LP004-6B	5531-6A	5531-6B
	LRL-2043	LRL-2044	LRL-2042	LRL-2045
	001f0102.d	001f0103.d	001f0101.d	001f0104.d
C20:4w6				
C20:3w3				
C20:4w3				
C20:5w3				
C22:0(1.000)	0.542	0.558	0.463	0.467
C22:1w11		0.038		
C22:1w9				
C22:1w7		0.034		
C21:5				
C23:0		0.029		
C22:4w6				
C22:5w6				
C22:5w3				
C24:0	0.373	0.391	0.280	0.283
C22:6w3	0.314	0.317	0.223	0.212
C24:1w9				
TOTAL	100.00	100.00	100.00	100.00

Table 16
Fatty Acid Profile

	5538-19A	5538-19B	LP004-6A	LP004-6B
	TRANSGENIC	TRANSGENIC	CONTROL	CONTROL
	LRL-2166	LRL-2167	LRL-2168	LRL-2169
C6:0	0.004	0.005		
C8:0	0.007	0.007	0.004	0.005
C10:0	0.012	0.012	0.008	0.008
C12:0	0.020	0.020	0.011	0.012
C13:0				
C14:0	0.099	0.108	0.050	0.050
C14:1w5				
C15:0	0.059	0.068	0.017	0.019
C16:0	5.272	5.294	4.049	4.057
C16:1	0.350	0.417	0.197	0.208
C16:2	0.199	0.187	0.076	0.077
C17:0	0.092	0.089	0.078	0.077
C16:3	0.149	0.149	0.192	0.198
C16:4		0.010		
C18:0	3.815	3.771	2.585	2.638
C18:1	57.562	57.051	68.506	68.352
C18:2 (6,9)	4.246	4.022		
C18:2w6	10.900	11.589	19.098	19.122
C18:2w3	0.020	0.008	0.008	0.009
C18:3w6	12.565	12.595	0.013	0.015
C18:3w3	1.084	1.137	1.501	1.542
C18:4	0.017	0.013	0.011	0.008
C18:4	0.028	0.024		
C20:0	1.138	1.104	0.937	0.943
C20:1	1.115	1.085	1.330	1.327
C20:2w6	0.150	0.143	0.068	0.071
C20:3w6	0.026	0.025	0.014	0.012
C20:4w6				
C20:3w3				

Table 16
Fatty Acid Profile

	5538-19A	5538-19B	LP004-6A	LP004-6B
	TRANSGENIC	TRANSGENIC	CONTROL	CONTROL
	LRL-2166	LRL-2167	LRL-2168	LRL-2169
C20:4w3				
C20:5w3				
C22:0	0.506	0.484	0.535	0.539
C22:1	0.017	0.020	0.032	0.032
C21:5		0.040	0.030	0.031
C22:4w6	0.038	0.064	0.015	0.014
C22:5w6				
C22:5w3	0.023	0.018	0.021	0.017
C24:0	0.352	0.321	0.353	0.362
C22:6w3	0.009			
C24:1w9	0.129	0.121	0.260	0.255
TOTAL	100.00	100.00	100.00	100.00

Example 15**Combined Expression of $\Delta 6$ and $\Delta 12$ Desaturases in *B. napus* Achieved by Crossing**

Plants containing either the $\Delta 6$ or the $\Delta 12$ desaturase were crossed and individual F1 half-seeds were analyzed for fatty acid composition by GC. Data from one such cross are given in Table 17. The parents for the cross were 5538-LP004-25-2-25 ($\Delta 6$ expressor) and 5542-SP30021-10-16 ($\Delta 12$ expressor). Reciprocal crosses were made and the results of 25 individual F1 seeds of each are shown in the table. Crosses are described such that the first parent indicated 10 is the female. Both sets of crosses gave approximately the same results. Compared to the parents, the $\Delta^{6,9}$ 18:2 decreased, and the GLA increased. $\Delta^{9,12}$ 18:2 levels are increased in most of the F1's as well. Note that these are F1 seeds and only contain one set of each desaturase. In future generations and selection of events homozygous for each desaturase, the F2 GLA levels 15 obtained may be even higher.

Combining traits by crossing may be preferable to combining traits on one T-DNA in some situations. Particularly if both genes are driven off of the same promoter (in this case napin), issues of promoter silencing may favor this approach over putting multiple cDNAs on one construct.

20 Alternatively, in some cases, combining multiple cDNAs on one T-DNA may be the method of choice. The results are shown in Table 17.

Table 17

STRAIN ID	16:0	16:1	18:0	18:1	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9	18:3_Δ9,12..	18:4	20:0	20:1
					12	11					
5538-LP004-25-2-25	4.23	0.13	2.4	61.78	8.77	6.34	11.58	0.92	0	0	0
5542-SP30021-10-16	4.09	0.1	2.03	38.4	0	41.88	0	11.06	0.02	0.75	1.03
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.9	0.04	2.31	38.58	0	27.91	20.94	2.67	0.65	0.92	1.28
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.5	0.04	1.88	36.24	0	28.68	22.54	3.36	0.85	0.78	1.32
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.51	0.03	1.98	38.36	0	29.48	19.95	3.06	0.68	0.79	1.38
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.95	0.04	1.86	38.65	0	28.08	20.81	2.92	0.75	0.76	1.42
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	4.26	0.05	2.44	40.25	0.01	28.81	18.08	2.74	0.53	0.88	1.24
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	4.13	0.04	2.33	34.48	0	26.73	26.2	2.32	0.75	0.9	1.27
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.8	0.04	2.15	38.34	0	28.95	20.64	2.63	0.65	0.81	1.3
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.96	0.05	1.59	36.43	0	29.05	21.85	3.47	0.86	0.68	1.32
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	4.04	0.04	2.5	37.75	0	27.23	22.89	1.95	0.55	0.99	1.26
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.53	0.04	1.8	34.88	0	29.17	23.42	3.42	0.9	0.74	1.3
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.43	0.04	1.89	37.12	0	29.52	20.91	3.35	0.8	0.79	1.35
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.58	0.03	2.55	39.54	0	28.81	19.34	2.44	0.54	0.98	1.34
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.53	0.03	2.33	39.26	0	29.07	19.5	2.61	0.59	0.91	1.37
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.4	0.02	2.41	45.53	0	28.94	13.71	2.51	0.37	0.91	1.44

Table 17

STRAIN ID	16:0	16:1	18:0	18:1	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9	18:3_Δ9,12	18:4	20:0	20:1
					<u>12</u>	<u>11</u>					
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.49	0.03	2.57	40.95	0	28.52	17.97	2.63	0.58	0.99	1.43
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.65	0.04	2.11	38.02	0	29.13	20.53	2.85	0.66	0.86	1.33
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.97	0.03	1.99	34.95	0.01	27.15	25.71	2.38	0.79	0.81	1.38
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.81	0.05	1.46	38.3	0	31.51	17.67	3.83	0.75	0.61	1.33
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.98	0.05	2.03	37.14	0	30.09	20.28	2.79	0.72	0.8	1.36
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	4.03	0.04	2.52	42.9	0	27.79	16.66	2.64	0.54	0.9	1.29
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	4.03	0.04	2.27	40.72	0	29.37	17.56	2.53	0.53	0.86	1.35
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.98	0.04	2.61	39.91	0	28.06	19.15	2.69	0.6	0.96	1.26
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	3.73	0.03	1.89	40.22	0	29.44	18.21	3	0.67	0.73	1.39
(5538-LP004-25-2-25 X 5542-SP30021-10-16)	4.02	0.04	2.14	42.58	0	30.36	15.18	2.43	0.42	0.82	1.3
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	4.14	0.06	2.23	30.67	0	30.38	25.47	3.12	0.91	0.9	1.29
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	4.05	0.07	1.7	37.03	0.04	32.1	15.97	5.38	0.96	0.69	1.28
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	4.01	0.07	1.58	38.02	0.05	33.65	13.92	5.15	0.89	0.66	1.28
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	4.07	0.06	2.01	31.63	0.05	31.13	23.09	3.94	1.1	0.83	1.28
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	4.03	0.05	1.94	31.88	0	30.98	23.71	3.45	0.99	0.82	1.3
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	3.92	0.06	1.71	35.77	0.03	33.15	16.39	5.28	0.98	0.68	1.32
(5542-SP30021-10-16 X 5538-LP004-25-2-25)	4.09	0.08	1.57	34.6	0.03	33.73	16.73	5.48	0.99	0.66	1.28

Table 17

STRAIN ID	16:0	16:1	18:0	18:1	18:2_Δ6,9	18:2_Δ9,12	18:3_Δ6,9, 12	18:3_Δ9,12, 11	18:4	20:0	20:1
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	3.94	0.07	1.59	34.03	0.04	31.35	19.76	5.29	1.22	0.67	1.28
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.13	0.06	1.85	31.44	0.06	31.28	23.77	3.52	1.04	0.79	1.22
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.14	0.06	1.96	31.11	0.04	31.88	23.3	3.6	1.01	0.82	1.27
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	3.98	0.07	1.58	35.06	0	32.06	18.1	5.33	1.12	0.67	1.28
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	3.89	0.06	1.59	32.51	0.05	29.44	22.91	5.33	1.54	0.67	1.25
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4	0.07	1.69	32.1	0.05	30.49	22.77	4.66	1.32	0.75	1.26
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.06	0.05	1.93	30.77	0.07	28.37	27.21	3.37	1.19	0.84	1.25
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.1	0.06	1.9	31.77	0.05	32.33	22.03	3.92	0.98	0.78	1.27
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	3.94	0.07	1.67	34.74	0.03	33.63	17.1	5.16	0.99	0.68	1.26
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	3.71	0.06	1.65	33.05	0	33.22	19.73	4.7	1.07	0.68	1.39
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	3.84	0.06	1.71	34.16	0.04	34.52	16.74	5.18	0.97	0.68	1.34
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4	0.07	1.66	34.97	0.07	33.08	17.07	5.27	1.1	0.67	1.28
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.16	0.06	1.99	35.44	0.05	31.89	18.95	3.68	0.89	0.81	1.29
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.05	0.08	1.46	33.49	0	31.96	18.81	6.2	1.32	0.61	1.28
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.2	0.06	1.93	35.06	0.06	33.69	17.38	4	0.86	0.78	1.21
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.07	0.06	1.74	36	0.06	32.18	17.86	4.32	0.96	0.73	1.27
(5542_SP30021-10-16 X 5538-LP004-25-2-25)	4.11	0.05	2.24	29.64	0.04	28.64	27.94	3.06	1.12	0.97	1.26

Example 16Expression of *M. alpina* desaturases in soybean

The *M. alpina* desaturases can be used to drive production of GLA and other PUFAs in soybean by use of the following expression constructs. Two means by which exogenous DNA can be inserted into the soybean genome are *Agrobacterium* infection or particle gun. Particle gun transformation is disclosed in U.S. patent 5,503,998. Plants can be selected using a glyphosate resistance marker (4, 971, 908). *Agrobacterium* transformation of soybean is well established to one of ordinary skill in the art.

For seed specific expression, the coding regions of the desaturase cDNAs are placed under control of the 5' regulatory region of *Glycine max* alpha-type beta conglycinin storage protein gene. The specific region that can be used is nucleotides 78-921 of gi 169928 (Doyle, J.J., Schuler, M.A., Godette, W.D., Zenger, V., Beachy, R.N., and Slightom. J.L., 1986 J. Biol. Chem. 261 (20), 9228-9238). The 3' regulatory region that can be used is from the pea ribulose 1,5 bisphosphate carboxylase/oxygenase small subunit (rbcS) gene. The specific sequences to be used are nucleotides 1-645 of gi 169145 (Hunt, A.G. 1988 DNA 7: 329-336).

Since soybean seeds contain more 18:2, and perhaps more endogenous Δ_{12} desaturase activity than *Brassica*, the effect of the *Mortierella* Δ_{12} desaturase on achieving optimal GLA levels can be tested as follows. A construct containing the Δ_6 cDNA can be used to see if $\Delta^{6,9}$ 18:2 is produced along with GLA. A construct containing the Δ_{12} desaturase can be used to see if the amount of 18:2 can be increased in soybean. A construct containing both the Δ_6 and Δ_{12} desaturases can be used to produce optimal levels of GLA. Alternatively, plants containing each of the single desaturases may be crossed if necessary to combine the genes.

Similar constructs may be made to express the Δ_5 desaturase alone, or in combination with Δ_{12} and/or Δ_6 desaturases.

Example 17Human Desaturase Gene Sequences

Human desaturase gene sequences potentially involved in long chain polyunsaturated fatty acid biosynthesis were isolated based on homology between the human cDNA sequences and *Mortierella alpina* desaturase gene sequences. The three conserved "histidine boxes" known to be conserved among membrane-bound desaturases were found. As with some other membrane-bound desaturases the final HXXHH histidine box motif was found to be QXXHH. The amino acid sequence of the putative human desaturases exhibited homology to *M. alpina* Δ5, Δ6, Δ9, and Δ12 desaturases.

The *M. alpina* Δ5 desaturase and Δ6 desaturase cDNA sequences were used to search the LifeSeq database of Incyte Pharmaceuticals, Inc., Palo Alto, California 94304. The Δ5 desaturase sequence was divided into fragments; 1) amino acid no. 1-150, 2) amino acid no. 151-300, and 3) amino acid no. 301-446. The Δ6 desaturase sequence was divided into three fragments; 1) amino acid no. 1-150, 2) amino acid no. 151-300, and 3) amino acid no. 301-457. These polypeptide fragments were searched against the database using the "tblastn" algorithm. This algorithm compares a protein query sequence against a nucleotide sequence database dynamically translated in all six reading frames (both strands).

The polypeptide fragments 2 and 3 of *M. alpina* Δ5 and Δ6 have homologies with the CloneID sequences as outlined in Table 18. The CloneID represents an individual sequence from the Incyte LifeSeq database. After the "tblastn" results have been reviewed, Clone Information was searched with the default settings of Stringency of >=50, and Productscore <=100 for different CloneID numbers. The Clone Information Results displayed the information including the ClusterID, CloneID, Library, HitID, Hit Description. When selected, the ClusterID number displayed the clone information of all the clones that belong in that ClusterID. The Assemble command assembles all of the CloneID which comprise the ClusterID. The following default settings were

used for GCG (Genetics Computer Group, University of Wisconsin Biotechnology Center, Madison, Wisconsin 53705) Assembly:

	Word Size:	7
5	Minimum Overlap:	14
	Stringency:	0.8
	Minimum Identity:	14
	Maximum Gap:	10
	Gap Weight:	8
10	Length Weight:	2

GCG Assembly Results displayed the contigs generated on the basis of sequence information within the CloneID. A contig is an alignment of DNA sequences based on areas of homology among these sequences. A new sequence (consensus sequence) was generated based on the aligned DNA sequences within a contig. The contig containing the CloneID was identified, and the ambiguous sites of the consensus sequence was edited based on the alignment of the CloneIDs (see SEQ ID NO:31 - SEQ ID NO:35) to generate the best possible sequence. The procedure was repeated for all six CloneID listed in Table 18. This produced five unique contigs. The edited consensus sequences of the 5 contigs were imported into the Sequencher software program (Gene Codes Corporation, Ann Arbor, Michigan 48105). These consensus sequences were assembled. The contig 2511785 overlaps with contig 3506132, and this new contig was called 2535 (SEQ ID NO:37). The contigs from the Sequencher program were copied into the Sequence Analysis software package of GCG.

Each contig was translated in all six reading frames into protein sequences. The *M. alpina* Δ5 (MA29) and Δ6 (MA524) sequences were compared with each of the translated contigs using the FastA search (a Pearson

and Lipman search for similarity between a query sequence and a group of sequences of the same type (nucleic acid or protein)). Homology among these sequences suggest the open reading frames of each contig. The homology among the *M. alpina* Δ5 and Δ6 to contigs 2535 and 3854933 were utilized to
5 create the final contig called 253538a. Figure 9 is the FastA match of the final contig 253538a and MA29, and Figure 10 is the FastA match of the final contig 253538a and MA524. The DNA sequences for the various contigs are presented in SEQ ID NO:31 -SEQ ID NO:37. The various peptide sequences are shown in SEQ ID NO:38 - SEQ ID NO: 44.

10 Although the open reading frame was generated by merging the two contigs, the contig 2535 shows that there is a unique sequence in the beginning of this contig which does not match with the contig 3854933. Therefore, it is possible that these contigs were generated from independent desaturase like human genes.

15 The contig 253538a contains an open reading frame encoding 432 amino acids. It starts with Gln (CAG) and ends with the stop codon (TGA). The contig 253538a aligns with both *M. alpina* Δ5 and Δ6 sequences, suggesting that it could be either of the desaturases, as well as other known desaturases which share homology with each other. The individual contigs listed in Table 18, as well as the intermediate contig 2535 and the final contig 20 253538a can be utilized to isolate the complete genes for human desaturases.

Uses of the Human Desaturases

These human sequences can be expressed in yeast and plants utilizing the procedures described in the preceding examples. For expression in
25 mammalian cells and transgenic animals, these genes may provide superior codon bias. In addition, these sequences can be used to isolate related desaturase genes from other organisms.

Table 18

Sections of the Desaturases	Clone ID from LifeSeq Database	Keyword
151-300 Δ5	3808675	fatty acid desaturase
301-446 Δ5	354535	Δ6
151-300 Δ6	3448789	Δ6
151-300 Δ6	1362863	Δ6
151-300 Δ6	2394760	Δ6
301-457 Δ6	3350263	Δ6

Example 18

5

Identification of Homologues to *M. alpina* Δ5 and Δ6 desaturases

A nucleic acid sequence that encodes a putative Δ5 desaturase was identified through a TBLASTN search of the expressed sequence tag databases through NCBI using amino acids 100-446 of Ma29 as a query. The truncated portion of the Ma29 sequence was used to avoid picking up homologies based on the cytochrome b5 portion at the N-terminus of the desaturase. The deduced amino acid sequence of an est from *Dictyostelium discoideum* (accession # C25549) shows very significant homology to Ma29 and lesser, but still significant homology to Ma524. The DNA sequence is presented as SEQ ID NO:45. The amino acid sequence is presented as SEQ ID NO:46.

15

Example 19**Identification of *M. alpina* Δ5 and Δ6 homologues in other PUFA-producing organisms**

To look for desaturases involved in PUFA production, a cDNA library was constructed from total RNA isolated from *Phaeodactylum tricornutum*. A plasmid-based cDNA library was constructed in pSPORT1 (GIBCO-BRL) following manufacturer's instructions using a commercially available kit (GIBCO-BRL). Random cDNA clones were sequenced and nucleic acid sequences that encode putative Δ5 or Δ6 desaturases were identified through BLAST search of the databases and comparison to Ma29 and Ma524 sequences.

One clone was identified from the *Phaeodactylum* library with homology to Ma29 and Ma524; it is called 144-011-B12. The DNA sequence is presented as SEQ ID NO:47. The amino acid sequence is presented as SEQ ID NO:48.

5

Example 20**Identification of *M. alpina* Δ5 and Δ6 homologues in other PUFA-producing organisms**

To look for desaturases involved in PUFA production, a cDNA library was constructed from total RNA isolated from *Schizochytrium* species. A 10 plasmid-based cDNA library was constructed in pSPORT1 (GIBCO-BRL) following manufacturer's instructions using a commercially available kit (GIBCO-BRL). Random cDNA clones were sequenced and nucleic acid sequences that encode putative Δ5 or Δ6 desaturases were identified through BLAST search of the databases and comparison to Ma29 and Ma524 sequences.

15

One clone was identified from the *Schizochytrium* library with homology to Ma29 and Ma524; it is called 81-23-C7. This clone contains a ~1 kb insert. Partial sequence was obtained from each end of the clone using the universal forward and reverse sequencing primers. The DNA sequence from the forward primer is presented as SEQ ID NO:49. The peptide sequence is 20 presented as SEQ ID NO:50. The DNA sequence from the reverse primer is presented as SEQ ID NO:51. The amino acid sequence from the reverse primer is presented as SEQ ID NO:52.

Example 21**Nutritional Compositions**

25 The PUFAs of the previous examples can be utilized in various nutritional supplements, infant formulations, nutritional substitutes and other nutrition solutions.

I. INFANT FORMULATIONS**A. Isomil® Soy Formula with Iron.**

Usage: As a beverage for infants, children and adults with an allergy or sensitivity to cow's milk. A feeding for patients with disorders for which lactose should be avoided: lactase deficiency, lactose intolerance and galactosemia.

5 Features:

- Soy protein isolate to avoid symptoms of cow's-milk-protein allergy or sensitivity
- Lactose-free formulation to avoid lactose-associated diarrhea
- Low osmolality (240 mOsm/kg water) to reduce risk of osmotic diarrhea.
- Dual carbohydrates (corn syrup and sucrose) designed to enhance carbohydrate absorption and reduce the risk of exceeding the absorptive capacity of the damaged gut.
- 1.8 mg of Iron (as ferrous sulfate) per 100 Calories to help prevent iron deficiency.
- Recommended levels of vitamins and minerals.
- Vegetable oils to provide recommended levels of essential fatty acids.
- Milk-white color, milk-like consistency and pleasant aroma.

20 Ingredients: (Pareve, ©) 85% water, 4.9% corn syrup, 2.6% sugar (sucrose), 2.1% soy oil, 1.9% soy protein isolate, 1.4% coconut oil, 0.15% calcium citrate, 0.11 % calcium phosphate tribasic, potassium citrate, potassium phosphate monobasic, potassium chloride, mono- and diglycerides, soy lecithin, carrageenan, ascorbic acid, L-methionine, magnesium chloride, potassium phosphate dibasic, sodium chloride, choline chloride, taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic

acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

B. Isomil® DF Soy Formula For Diarrhea.

5 Usage: As a short-term feeding for the dietary management of diarrhea
in infants and toddlers.

Features:

- First infant formula to contain added dietary fiber from soy fiber specifically for diarrhea management.
- Clinically shown to reduce the duration of loose, watery stools during mild to severe diarrhea in infants.
- Nutritionally complete to meet the nutritional needs of the infant.
- Soy protein isolate with added L-methionine meets or exceeds an infant's requirement for all essential amino acids.
- Lactose-free formulation to avoid lactose-associated diarrhea.
- Low osmolality (240 mOsm/kg water) to reduce the risk of osmotic diarrhea.
- Dual carbohydrates (corn syrup and sucrose) designed to enhance carbohydrate absorption and reduce the risk of exceeding the absorptive capacity of the damaged gut.
- Meets or exceeds the vitamin and mineral levels recommended by the Committee on Nutrition of the American Academy of Pediatrics and required by the Infant Formula Act.
- 1.8 mg of iron (as ferrous sulfate) per 100 Calories to help prevent iron deficiency.
- Vegetable oils to provide recommended levels of essential fatty acids.

25 Ingredients: (Pareve, ®) 86% water, 4.8% corn syrup, 2.5% sugar (sucrose), 2.1% soy oil, 2.0% soy protein isolate, 1.4% coconut oil, 0.77% soy

fiber, 0.12% calcium citrate, 0.11 % calcium phosphate tribasic, 0.10% potassium citrate, potassium chloride, potassium phosphate monobasic, mono- and disglycerides, soy lecithin, carrageenan, magnesium chloride, ascorbic acid, L-methionine, potassium phosphate dibasic, sodium chloride, choline chloride, 5 taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

10 **C. Isomil® SF Sucrose-Free Soy Formula With Iron.**

Usage: As a beverage for infants, children and adults with an allergy or sensitivity to cow's-milk protein or an intolerance to sucrose. A feeding for patients with disorders for which lactose and sucrose should be avoided.

Features:

- 15 • Soy protein isolate to avoid symptoms of cow's-milk-protein allergy or sensitivity.
- Lactose-free formulation to avoid lactose-associated diarrhea (carbohydrate source is Polycose® Glucose Polymers).
- Sucrose free for the patient who cannot tolerate sucrose.
- 20 • Low osmolality (180 mOsm/kg water) to reduce risk of osmotic diarrhea.
- 1.8 mg of iron (as ferrous sulfate) per 100 Calories to help prevent iron deficiency.
- Recommended levels of vitamins and minerals.
- 25 • Vegetable oils to provide recommended levels of essential fatty acids.
- Milk-white color, milk-like consistency and pleasant aroma.

Ingredients: (Pareve, ©) 75% water, 11.8% hydrolized cornstarch, 4.1% soy oil, 4.1% soy protein isolate, 2.8% coconut oil, 1.0% modified cornstarch,

0.38% calcium phosphate tribasic, 0.17% potassium citrate, 0.13% potassium chloride, mono- and disglycerides, soy lecithin, magnesium chloride, ascorbic acid, L-methionine, calcium carbonate, sodium chloride, choline chloride, carrageenan, taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

5 **D. Isomil® 20 Soy Formula With Iron Ready To Feed,
10 20 Cal/fl oz.**

Usage: When a soy feeding is desired.

Ingredients: (Pareve, ©) 85% water, 4.9% corn syrup, 2.6% sugar (sucrose), 2.1% soy oil, 1.9% soy protein isolate, 1.4% coconut oil, 0.15% calcium citrate, 0.11% calcium phosphate tribasic, potassium citrate, potassium phosphate monobasic, potassium chloride, mono- and disglycerides, soy lecithin, carrageenan, ascorbic acid, L-methionine, magnesium chloride, potassium phosphate dibasic, sodium chloride, choline chloride, taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

15 **E. Similac® Infant Formula**

20 Usage: When an infant formula is needed: if the decision is made to discontinue breastfeeding before age 1 year, if a supplement to breastfeeding is needed or as a routine feeding if breastfeeding is not adopted.

Features:

- Protein of appropriate quality and quantity for good growth; heat-denatured, which reduces the risk of milk-associated enteric blood loss.
- 5 • Fat from a blend of vegetable oils (doubly homogenized), providing essential linoleic acid that is easily absorbed.
- Carbohydrate as lactose in proportion similar to that of human milk.
- Low renal solute load to minimize stress on developing organs.
- 10 • Powder, Concentrated Liquid and Ready To Feed forms.

Ingredients: (®-D) Water, nonfat milk, lactose, soy oil, coconut oil, mono- and diglycerides, soy lecithin, ascorbic acid, carrageenan, choline chloride, taurine, m-inositol, alpha-tocopheryl acetate, zinc sulfate, niacinamide, ferrous sulfate, calcium pantothenate, cupric sulfate, vitamin A palmitate, 15 thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

F. Similac® NeoCare Premature Infant Formula With Iron

Usage: For premature infants' special nutritional needs after hospital discharge. Similac NeoCare is a nutritionally complete formula developed to provide premature infants with extra calories, protein, vitamins and minerals needed to promote catch-up growth and support development.

Features:

- Reduces the need for caloric and vitamin supplementation. More calories (22 Cal/fl oz) than standard term formulas (20 Cal/fl oz).
- 25 • Highly absorbed fat blend, with medium-chain triglycerides (MCT oil) to help meet the special digestive needs of premature infants.
- Higher levels of protein, vitamins and minerals per 100 Calories to extend the nutritional support initiated in-hospital.

- More calcium and phosphorus for improved bone mineralization.

Ingredients: ④-D Corn syrup solids, nonfat milk, lactose, whey protein concentrate, soy oil, high-oleic safflower oil, fractionated coconut oil (medium-chain triglycerides), coconut oil, potassium citrate, calcium phosphate tribasic, 5 calcium carbonate, ascorbic acid, magnesium chloride, potassium chloride, sodium chloride, taurine, ferrous sulfate, m-inositol, choline chloride, ascorbyl palmitate, L-carnitine, alpha-tocopheryl acetate, zinc sulfate, niacinamide, mixed tocopherols, sodium citrate, calcium pantothenate, cupric sulfate, thiamine chloride hydrochloride, vitamin A palmitate, beta carotene, riboflavin, 10 pyridoxine hydrochloride, folic acid, manganese sulfate, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

G. Similac Natural Care Low-Iron Human Milk Fortifier Ready To Use, 24 Cal/fl oz.

Usage: Designed to be mixed with human milk or to be fed alternatively 15 with human milk to low-birth-weight infants.

Ingredients: ④-D Water, nonfat milk, hydrolyzed cornstarch, lactose, fractionated coconut oil (medium-chain triglycerides), whey protein concentrate, soy oil, coconut oil, calcium phosphate tribasic, potassium citrate, magnesium chloride, sodium citrate, ascorbic acid, calcium carbonate, mono- 20 and diglycerides, soy lecithin, carrageenan, choline chloride, m-inositol, taurine, niacinamide, L-carnitine, alpha tocopheryl acetate, zinc sulfate, potassium chloride, calcium pantothenate, ferrous sulfate, cupric sulfate, riboflavin, vitamin A palmitate, thiamine chloride hydrochloride, pyridoxine hydrochloride, biotin, folic acid, manganese sulfate, phylloquinone, vitamin D₃, 25 sodium selenite and cyanocobalamin.

Various PUFAs of this invention can be substituted and/or added to the infant formulae described above and to other infant formulae known to those in the art..

II. NUTRITIONAL FORMULATIONS

A. ENSURE®

Usage: ENSURE is a low-residue liquid food designed primarily as an oral nutritional supplement to be used with or between meals or, in appropriate amounts, as a meal replacement. ENSURE is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets. Although it is primarily an oral supplement, it can be fed by tube.

Patient Conditions:

- For patients on modified diets
- For elderly patients at nutrition risk
- For patients with involuntary weight loss
- For patients recovering from illness or surgery
- For patients who need a low-residue diet

Ingredients:

④-D Water, Sugar (Sucrose), Maltodextrin (Corn), Calcium and Sodium Caseinates, High-Oleic Safflower Oil, Soy Protein Isolate, Soy Oil, Canola Oil, Potassium Citrate, Calcium Phosphate Tribasic, Sodium Citrate, Magnesium Chloride, Magnesium Phosphate Dibasic, Artificial Flavor, Sodium Chloride, Soy Lecithin, Choline Chloride, Ascorbic Acid, Carrageenan, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Gellan Gum, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Folic Acid, Sodium Molybdate, Chromium Chloride, Biotin, Potassium Iodide, Sodium Selenate.

B. ENSURE® BARS

Usage: ENSURE BARS are complete, balanced nutrition for supplemental use between or with meals. They provide a delicious, nutrient-

rich alternative to other snacks. ENSURE BARS contain <1 g lactose/bar, and Chocolate Fudge Brownie flavor is gluten-free. (Honey Graham Crunch flavor contains gluten.)

Patient Conditions:

- 5 • For patients who need extra calories, protein, vitamins and minerals
• Especially useful for people who do not take in enough calories and nutrients
• For people who have the ability to chew and swallow
• Not to be used by anyone with a peanut allergy or any type of allergy to nuts.

Ingredients:

Honey Graham Crunch -- High-Fructose Corn Syrup, Soy Protein-Isolate, Brown Sugar, Honey, Maltodextrin (Corn), Crisp Rice (Milled Rice, Sugar [Sucrose], Salt [Sodium Chloride] and Malt), Oat Bran, Partially Hydrogenated Cottonseed and Soy Oils, Soy Polysaccharide, Glycerine, Whey Protein Concentrate, Polydextrose, Fructose, Calcium Caseinate, Cocoa Powder, Artificial Flavors, Canola Oil, High-Oleic Safflower Oil, Nonfat Dry Milk, Whey Powder, Soy Lecithin and Corn Oil. Manufactured in a facility that processes nuts.

20 **Vitamins and Minerals:**

Calcium Phosphate Tribasic, Potassium Phosphate Dibasic, Magnesium Oxide, Salt (Sodium Chloride), Potassium Chloride, Ascorbic Acid, Ferric Orthophosphate, Alpha-Tocopheryl Acetate, Niacinamide, Zinc Oxide, Calcium Pantothenate, Copper Gluconate, Manganese Sulfate, Riboflavin, Beta-Carotene, Pyridoxine Hydrochloride, Thiamine Mononitrate, Folic Acid, Biotin, Chromium Chloride, Potassium Iodide, Sodium Selenate, Sodium Molybdate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein:

Honey Graham Crunch - The protein source is a blend of soy protein isolate and milk proteins.

5	Soy protein isolate	74%
	Milk proteins	26%

Fat:

Honey Graham Crunch - The fat source is a blend of partially hydrogenated cottonseed and soybean, canola, high oleic safflower, and corn oils, and soy lecithin.

10	Partially hydrogenated cottonseed and soybean oil	76%
	Canola oil	8%
	High-oleic safflower oil	8%
	Corn oil	4%
	Soy lecithin	4%

Carbohydrate:

Honey Graham Crunch - The carbohydrate source is a combination of high-fructose corn syrup, brown sugar, maltodextrin, honey, crisp rice, glycerine, soy polysaccharide, and oat bran.

20	High-fructose corn syrup	24%
	Brown sugar	21%
	Maltodextrin	12%
	Honey	11%
	Crisp rice	9%
	Glycerine	9%
25	Soy polysaccharide	7%
	Oat bran	7%\

C. ENSURE® HIGH PROTEIN

Usage: ENSURE HIGH PROTEIN is a concentrated, high-protein liquid food designed for people who require additional calories, protein, vitamins, and minerals in their diets. It can be used as an oral nutritional supplement with or between meals or, in appropriate amounts, as a meal replacement. ENSURE HIGH PROTEIN is lactose- and gluten-free, and is suitable for use by people recovering from general surgery or hip fractures and by patients at risk for pressure ulcers.

- Patient Conditions
- 10 • For patients who require additional calories, protein, vitamins, and minerals, such as patients recovering from general surgery or hip fractures, patients at risk for pressure ulcers, and patients on low-cholesterol diets

- Features-
- 15 • Low in saturated fat
 - Contains 6 g of total fat and < 5 mg of cholesterol per serving
 - Rich, creamy taste
 - Excellent source of protein, calcium, and other essential vitamins and minerals
 - For low-cholesterol diets
 - 20 • Lactose-free, easily digested

Ingredients:

Vanilla Supreme: -⁰-D Water, Sugar (Sucrose), Maltodextrin (Corn), Calcium and Sodium Caseinates, High-Oleic Safflower Oil, Soy Protein Isolate, Soy Oil, Canola Oil, Potassium Citrate, Calcium Phosphate Tribasic, Sodium Citrate, Magnesium Chloride, Magnesium Phosphate Dibasic, Artificial Flavor, Sodium Chloride, Soy Lecithin, Choline Chloride, Ascorbic Acid, Carrageenan, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Gellan Gum, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride,

Riboflavin, Folio Acid, Sodium Motybdate, Chromium Chloride, Biotin, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D.3 and Cyanocobalamin.

Protein:

- 5 The protein source is a blend of two high-biologic-value proteins: casein and soy.

Sodium and calcium caseinates	85%
Soy protein isolate	15%

Fat:

- 10 The fat source is a blend of three oils: high-oleic safflower, canola, and soy.

High-oleic safflower oil	40%
Canola oil	30%
Soy oil	30%

- 15 The level of fat in ENSURE HIGH PROTEIN meets American Heart Association (AHA) guidelines. The 6 grams of fat in ENSURE HIGH PROTEIN represent 24% of the total calories, with 2.6% of the fat being from saturated fatty acids and 7.9% from polyunsaturated fatty acids. These values are within the AHA guidelines of \leq 30% of total calories from fat, < 1 0% of the calories from saturated fatty acids, and \leq 1 0% of total calories from polyunsaturated fatty acids.
- 20

Carbohydrate:

- 25 ENSURE HIGH PROTEIN contains a combination of maltodextrin and sucrose. The mild sweetness and flavor variety (vanilla supreme, chocolate royal, wild berry, and banana), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla and other nonchocolate flavors

Sucrose	60%
---------	-----

Maltodextrin	40%
Chocolate	
Sucrose	70%
Maltodextrin	30%

5

D. ENSURE ® LIGHT

Usage: ENSURE LIGHT is a low-fat liquid food designed for use as an oral nutritional supplement with or between meals. ENSURE LIGHT is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets.

10

Patient Conditions:

- For normal-weight or overweight patients who need extra nutrition in a supplement that contains 50% less fat and 20% fewer calories than ENSURE
- For healthy adults who don't eat right and need extra nutrition

15

Features:

- Low in fat and saturated fat
- Contains 3 g of total fat per serving and < 5 mg cholesterol
- Rich, creamy taste
- Excellent source of calcium and other essential vitamins and minerals
- For low-cholesterol diets
- Lactose-free, easily digested

20

Ingredients:

25

French Vanilla: ©-D Water, Maltodextrin (Corn), Sugar (Sucrose), Calcium Caseinate, High-Oleic Safflower Oil, Canola Oil, Magnesium Chloride, Sodium Citrate, Potassium Citrate, Potassium Phosphate Dibasic, Magnesium Phosphate Dibasic, Natural and Artificial Flavor, Calcium Phosphate Tribasic, Cellulose Gel, Choline Chloride, Soy Lecithin, Carrageenan, Salt (Sodium Chloride),

Ascorbic Acid, Cellulose Gum, Ferrous Sulfate, Alpha-Tocopheryl Acetate,
Zinc Sulfate, Niacinamide, Manganese Sulfate, Calcium Pantothenate, Cupric
Sulfate, Thiamine Chloride Hydrochloride, Vitamin A Palmitate, Pyridoxine
Hydrochloride, Riboflavin, Chromium Chloride, Folic Acid, Sodium
5 Molybdate, Biotin, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin
D₃ and Cyanocobalamin.

Protein:

The protein source is calcium caseinate.

Calcium caseinate	100%
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10 **Fat**

The fat source is a blend of two oils: high-oleic safflower and canola.

High-oleic safflower oil	70%
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Canola oil	30%
------------	-----

15 The level of fat in ENSURE LIGHT meets American Heart Association (AHA) guidelines. The 3 grams of fat in ENSURE LIGHT represent 13.5% of the total calories, with 1.4% of the fat being from saturated fatty acids and 2.6% from polyunsaturated fatty acids. These values are within the AHA guidelines of \leq 30% of total calories from fat, < 10% of the calories from saturated fatty acids, and \leq 10% of total calories from polyunsaturated fatty acids.

20 **Carbohydrate**

ENSURE LIGHT contains a combination of maltodextrin and sucrose. The chocolate flavor contains corn syrup as well. The mild sweetness and flavor variety (French vanilla, chocolate supreme, strawberry swirl), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

25 **Vanilla and other nonchocolate flavors**

Sucrose	51%
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Maltodextrin	49%
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Chocolate

Sucrose	47.0%
Corn Syrup	26.5%
Maltodextrin	26.5%

5 **Vitamins and Minerals**

An 8-fl-oz serving of ENSURE LIGHT provides at least 25% of the RDIs for 24 key vitamins and minerals.

Caffeine

Chocolate flavor contains 2.1 mg caffeine/8 fl oz.

10

E. ENSURE PLUS®

Usage: ENSURE PLUS is a high-calorie, low-residue liquid food for use when extra calories and nutrients, but a normal concentration of protein, are needed. It is designed primarily as an oral nutritional supplement to be used with or between meals or, in appropriate amounts, as a meal replacement. ENSURE PLUS is lactose- and gluten-free. Although it is primarily an oral nutritional supplement, it can be fed by tube.

Patient Conditions:

- 20 • For patients who require extra calories and nutrients, but a normal concentration of protein, in a limited volume
- For patients who need to gain or maintain healthy weight

Features

- Rich, creamy taste
- Good source of essential vitamins and minerals

25 **Ingredients**

Vanilla: ©-D Water, Corn Syrup, Maltodextrin (Corn), Corn Oil, Sodium and Calcium Caseinates, Sugar (Sucrose), Soy Protein Isolate, Magnesium Chloride,

Potassium Citrate, Calcium Phosphate Tribasic, Soy Lecithin, Natural and Artificial Flavor, Sodium Citrate, Potassium Chloride, Choline Chloride, Ascorbic Acid, Carrageenan, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Vitamin A Palmitate, Folic Acid, Biotin, Chromium Chloride, Sodium Molybdate, Potassium Iodide, Sodium Selenite, Phylloquinone, Cyanocobalamin and Vitamin D₃.

5

Protein

10

The protein source is a blend of two high-biologic-value proteins: casein and soy.

Sodium and calcium caseinates	84%
Soy protein isolate	16%

Fat

15

The fat source is corn oil.

Corn oil	100%
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Carbohydrate

20

ENSURE PLUS contains a combination of maltodextrin and sucrose. The mild sweetness and flavor variety (vanilla, chocolate, strawberry, coffee, buffer pecan, and eggnog), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla, strawberry, butter pecan, and coffee flavors

25

Corn Syrup	39%
Maltodextrin	38%
Sucrose	23%

Chocolate and eggnog flavors

Corn Syrup	36%
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Maltodextrin	34%
Sucrose	30%

Vitamins and Minerals

An 8-fl-oz serving of ENSURE PLUS provides at least 15% of the RDIs
5 for 25 key Vitamins and minerals.

Caffeine

Chocolate flavor contains 3.1 mg Caffeine/8 fl oz. Coffee flavor
contains a trace amount of caffeine.

10 **F. ENSURE PLUS® HN**

Usage: ENSURE PLUS HN is a nutritionally complete high-calorie,
high-nitrogen liquid food designed for people with higher calorie and protein
needs or limited volume tolerance. It may be used for oral supplementation or
for total nutritional support by tube. ENSURE PLUS HN is lactose- and gluten-
15 free.

Patient Conditions:

- For patients with increased calorie and protein needs, such as following surgery or injury
- For patients with limited volume tolerance and early satiety

20 **Features**

- For supplemental or total nutrition
- For oral or tube feeding
- 1.5 CaVmL
- High nitrogen
- Calorically dense

Ingredients

Vanilla: ©-D Water, Maltodextrin (Corn), Sodium and Calcium Caseinates, Corn Oil, Sugar (Sucrose), Soy Protein Isolate, Magnesium Chloride, Potassium Citrate, Calcium Phosphate Tribasic, Soy Lecithin, Natural and Artificial 5 Flavor, Sodium Citrate, Choline Chloride, Ascorbic Acid, Taurine, L-Carnitine, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Niacinamide, Carrageenan, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Vitamin A Palmitate, Folic Acid, Biotin, Chromium Chloride, Sodium 10 Molybdate, Potassium Iodide, Sodium Selenite, Phylloquinone, Cyanocobalamin and Vitamin D₃.

G. ENSURE® POWDER

Usage: ENSURE POWDER (reconstituted with water) is a low-residue 15 liquid food designed primarily as an oral nutritional supplement to be used with or between meals. ENSURE POWDER is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets.

Patient Conditions:

- For patients on modified diets
- 20 • For elderly patients at nutrition risk
- For patients recovering from illness/surgery
- For patients who need a low-residue diet

Features

- Convenient, easy to mix
- 25 • Low in saturated fat
- Contains 9 g of total fat and < 5 mg of cholesterol per serving
- High in vitamins and minerals
- For low-cholesterol diets

- Lactose-free, easily digested

Ingredients: D-Corn Syrup, Maltodextrin (Corn), Sugar (Sucrose), Corn Oil, Sodium and Calcium Caseinates, Soy Protein Isolate, Artificial Flavor, Potassium Citrate, Magnesium Chloride, Sodium Citrate, Calcium Phosphate Tribasic, Potassium Chloride, Soy Lecithin, Ascorbic Acid, Choline Chloride, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Thiamine Chloride Hydrochloride, Cupric Sulfate, Pyridoxine Hydrochloride, Riboflavin, Vitamin A Palmitate, Folic Acid, Biotin, Sodium Molybdate, Chromium Chloride, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein

The protein source is a blend of two high-biologic-value proteins: casein and soy.

	Sodium and calcium caseinates	84%
15	Soy protein isolate	16%

Fat

The fat source is corn oil.

Corn oil	100%
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Carbohydrate

20 ENSURE POWDER contains a combination of corn syrup, maltodextrin, and sucrose. The mild sweetness of ENSURE POWDER, plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, helps to prevent flavor fatigue and aid in patient compliance.

Vanilla

25	Corn Syrup	35%
	Maltodextrin	35%
	Sucrose	30%

H. ENSURE® PUDDING

Usage: ENSURE PUDDING is a nutrient-dense supplement providing balanced nutrition in a nonliquid form to be used with or between meals. It is appropriate for consistency-modified diets (e.g., soft, pureed, or full liquid) or
5 for people with swallowing impairments. ENSURE PUDDING is gluten-free.

Patient Conditions:

- For patients on consistency-modified diets (e.g., soft, pureed, or full liquid)
- For patients with swallowing impairments

Features

- 10 • Rich and creamy, good taste
- Good source of essential vitamins and minerals Convenient-needs no refrigeration
- Gluten-free

15 Nutrient Profile per 5 oz: Calories 250, Protein 10.9%, Total Fat 34.9%, Carbohydrate 54.2%

Ingredients:

Vanilla: ©-D Nonfat Milk, Water, Sugar (Sucrose), Partially Hydrogenated Soybean Oil, Modified Food Starch, Magnesium Sulfate. Sodium Stearoyl Lactylate, Sodium Phosphate Dibasic, Artificial Flavor, Ascorbic Acid, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Choline Chloride, Niacinamide, Manganese Sulfate, Calcium Pantothenate, FD&C Yellow #5, Potassium Citrate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, FD&C Yellow #6, Folic Acid, Biotin, Phylloquinone, Vitamin D3 and Cyanocobalamin.
20

25 Protein

The protein source is nonfat milk.

Nonfat milk	100%
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Fat

The fat source is hydrogenated soybean oil.

Hydrogenated soybean oil 100%

Carbohydrate

5 ENSURE PUDDING contains a combination of sucrose and modified food starch. The mild sweetness and flavor variety (vanilla, chocolate, butterscotch, and tapioca) help prevent flavor fatigue. The product contains 9.2 grams of lactose per serving.

Vanilla and other nonchocolate flavors

10 Sucrose 56%
 Lactose 27%
 Modified food starch 17%

Chocolate

15 Sucrose 58%
 Lactose 26%
 Modified food starch 16%

I. ENSURE® WITH FIBER

Usage: ENSURE WITH FIBER is a fiber-containing, nutritionally complete liquid food designed for people who can benefit from increased dietary fiber and nutrients. ENSURE WITH FIBER is suitable for people who do not require a low-residue diet. It can be fed orally or by tube, and can be used as a nutritional supplement to a regular diet or, in appropriate amounts, as a meal replacement. ENSURE WITH FIBER is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets.

Patient Conditions

- For patients who can benefit from increased dietary fiber and nutrients

Features

- New advanced formula-low in saturated fat, higher in vitamins and minerals
- Contains 6 g of total fat and < 5 mg of cholesterol per serving
- Rich, creamy taste
- 5 • Good source of fiber
- Excellent source of essential vitamins and minerals
- For low-cholesterol diets
- Lactose- and gluten-free

Ingredients

10 **Vanilla:** ©-D Water, Maltodextrin (Corn), Sugar (Sucrose), Sodium and Calcium Caseinates, Oat Fiber, High-Oleic Safflower Oil, Canola Oil, Soy Protein Isolate, Corn Oil, Soy Fiber, Calcium Phosphate Tribasic, Magnesium Chloride, Potassium Citrate, Cellulose Gel, Soy Lecithin, Potassium Phosphate Dibasic, Sodium Citrate, Natural and Artificial Flavors, Choline Chloride, 15 Magnesium Phosphate, Ascorbic Acid, Cellulose Gum, Potassium Chloride, Carrageenan, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Zinc Sulfate, Niacinamide, Manganese Sulfate, Calcium Pantothenate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Folic Acid, Chromium Chloride, Biotin, Sodium 20 Molybdate, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein

The protein source is a blend of two high-biologic-value proteins- casein and soy.

25	Sodium and calcium caseinates	80%
	Soy protein isolate	20%

Fat

The fat source is a blend of three oils: high-oleic safflower, canola, and corn.

	High-oleic safflower oil	40%
5	Canola oil	40%
	Corn oil	20%

The level of fat in ENSURE WITH FIBER meets American Heart Association (AHA) guidelines. The 6 grams of fat in ENSURE WITH FIBER represent 22% of the total calories, with 2.01 % of the fat being from saturated fatty acids and 6.7% from polyunsaturated fatty acids. These values are within the AHA guidelines of \leq 30% of total calories from fat, < 1 0% of the calories from saturated fatty acids, and \leq 1 0% of total calories from polyunsaturated fatty acids.

Carbohydrate

15 ENSURE WITH FIBER contains a combination of maltodextrin and sucrose. The mild sweetness and flavor variety (vanilla, chocolate, and butter pecan), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla and other nonchocolate flavors

20	Maltodextrin	66%
	Sucrose	25%
	Oat Fiber	7%
	Soy Fiber	2%

Chocolate

25	Maltodextrin	55%
	Sucrose	36%
	Oat Fiber	7%

Fiber

Soy Fiber	2%
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The fiber blend used in ENSURE WITH FIBER consists of oat fiber and soy polysaccharide. This blend results in approximately 4 grams of total dietary fiber per 8-fl-oz can. The ratio of insoluble to soluble fiber is 95:5.

The various nutritional supplements described above and known to others of skill in the art can be substituted and/or supplemented with the PUFAs of this invention.

J. Oxepa™ Nutritional Product

10 Oxepa is low-carbohydrate, calorically dense enteral nutritional product designed for the dietary management of patients with or at risk for ARDS. It has a unique combination of ingredients, including a patented oil blend containing eicosapentaenoic acid (EPA from fish oil), γ -linolenic acid (GLA from borage oil), and elevated antioxidant levels.

15 Caloric Distribution:

- Caloric density is high at 1.5 Cal/mL (355 Cal/8 fl oz), to minimize the volume required to meet energy needs.
 - The distribution of Calories in Oxepa is shown in Table 7.

Table 7. Caloric Distribution of Oxepa			
	per 8 fl oz.	per liter	% of Cal
Calories	355	1,500	---
Fat (g)	22.2	93.7	55.2
Carbohydrate (g)	25	105.5	28.1
Protein (g)	14.8	62.5	16.7
Water (g)	186	785	---

20 **Fat:**

- Oxepa contains 22.2 g of fat per 8-fl oz serving (93.7 g/L).
 - The fat source is a oil blend of 31.8% canola oil, 25% medium-chain triglycerides (MCTs), 20% borage oil, 20% fish oil, and 3.2 % soy lecithin. The typical fatty acid profile of Oxepa is shown in Table 8.

- Oxepa provides a balanced amount of polyunsaturated, monounsaturated, and saturated fatty acids, as shown in Table 10.
 - Medium-chain triglycerides (MCTs) -- 25% of the fat blend -- aid gastric emptying because they are absorbed by the intestinal tract without emulsification by bile acids.
- 5

The various fatty acid components of Oxepa™ nutritional product can be substituted and/or supplemented with the PUFAs of this invention.

Table 8. Typical Fatty Acid Profile			
	% Total Fatty Acids	g/8 fl oz*	g/L*
Caproic (6:0)	0.2	0.04	0.18
Caprylic (8:0)	14.69	3.1	13.07
Capric (10:0)	11.06	2.33	9.87
Palmitic (16:0)	5.59	1.18	4.98
Palmitoleic (16:1n-7)	1.82	0.38	1.62
Stearic (18:0)	1.84	0.39	1.64
Oleic (18:1n-9)	24.44	5.16	21.75
Linoleic (18:2n-6)	16.28	3.44	14.49
α-Linolenic (18:3n-3)	3.47	0.73	3.09
γ-Linolenic (18:3n-6)	4.82	1.02	4.29
Eicosapentaenoic (20:5n-3)	5.11	1.08	4.55
n-3-Docosapentaenoic (22:5n-3)	0.55	0.12	0.49
Docosahexaenoic (22:6n-3)	2.27	0.48	2.02
Others	7.55	1.52	6.72

* Fatty acids equal approximately 95% of total fat.

Table 9. Fat Profile of Oxepa.	
% of total calories from fat	55.2
Polyunsaturated fatty acids	31.44 g/L
Monounsaturated fatty acids	25.53 g/L
Saturated fatty acids	32.38 g/L
n-6 to n-3 ratio	1.75:1
Cholesterol	9.49 mg/8 fl oz 40.1 mg/L

Carbohydrate:

- The carbohydrate content is 25.0 g per 8-fl-oz serving (105.5 g/L).
 - The carbohydrate sources are 45% maltodextrin (a complex carbohydrate) and 55% sucrose (a simple sugar), both of which are readily digested and absorbed.
- 5
- The high-fat and low-carbohydrate content of Oxepa is designed to minimize carbon dioxide (CO₂) production. High CO₂ levels can complicate weaning in ventilator-dependent patients. The low level of carbohydrate also may be useful for those patients who have developed stress-induced hyperglycemia.
- 10
- Oxepa is lactose-free.

Dietary carbohydrate, the amino acids from protein, and the glycerol moiety of fats can be converted to glucose within the body. Throughout this process, the carbohydrate requirements of glucose-dependent tissues (such as the central nervous system and red blood cells) are met. However, a diet free of carbohydrates can lead to ketosis, excessive catabolism of tissue protein, and loss of fluid and electrolytes. These effects can be prevented by daily ingestion of 50 to 100 g of digestible carbohydrate, if caloric intake is adequate. The carbohydrate level in Oxepa is also sufficient to minimize gluconeogenesis, if energy needs are being met.

15

20

Protein:

- Oxepa contains 14.8 g of protein per 8-fl-oz serving (62.5 g/L).
 - The total calorie/nitrogen ratio (150:1) meets the need of stressed patients.
 - Oxepa provides enough protein to promote anabolism and the maintenance of lean body mass without precipitating respiratory problems. High protein intakes are a concern in patients with respiratory insufficiency. Although protein has little effect on CO₂ production, a high protein diet will increase ventilatory drive.
- 25

- The protein sources of Oxepa are 86.8% sodium caseinate and 13.2% calcium caseinate.
- As demonstrated in Table 11, the amino acid profile of the protein system in Oxepa meets or surpasses the standard for high quality protein set by
5 the National Academy of Sciences.
- Oxepa is gluten-free.

All publications and patent applications mentioned in this specification
are indicative of the level of skill of those skilled in the art to which this
10 invention pertains. All publications and patent applications are herein
incorporated by reference to the same extent as if each individual publication or
patent application was specifically and individually indicated to be incorporated
by reference.

The invention now being fully described, it will be apparent to one of
15 ordinary skill in the art that many changes and modifications can be made
thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

- (i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
- (iii) NUMBER OF SEQUENCES: 52
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LIMBACH & LIMBACH L.L.P.
(B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/834,033
(B) FILING DATE: 11-APR-1997
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/833,610
(B) FILING DATE: 11-APR-1997
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: MICHAEL R. WARD
(B) REGISTRATION NUMBER: 38,351
(C) REFERENCE/DOCKET NUMBER: CGAB-320
- (x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 433-4150
(B) TELEFAX: (415) 433-8716
(C) TELEX: N/A

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	CGACACTCCT TCCTTCTTCT CACCCGTCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG	60
15	ACAACAAACC ATGGCTGCTG CTCCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTGAA	120
	TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA	180
20	CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT	240
	CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTCACCCCCG AGGCTGCTTG	300
25	GGAGACTCTT GCCAACTTTT ACGTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA	360
	TGATGACTTT CGGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA	420
30	CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT	480
	GTCGACGGTC ATTGTGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGC	540
35	TGCGCTTTG GGTCTGTTCT GGCAGCAGTG CGGATGGTTG GCTCACGACT TTTTGATCA	600
	CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTCTGGC GCCTTCTTGG GAGGTGTCTG	660
40	CCAGGGCTTC TCGTCCTCGT GGTGGAAGGA CAAGCACAAAC ACTCACCAACG CCGCCCCAA	720
	CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCCTTG TTGACCTGGA GTGAGCATGC	780
45	GTTGGAGATG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT	840
	GGTCCTGAAC CAGACCTGGT TTTACTTCCC CATTCTCTCG TTTGCCGTC TCTCCTGGT	900
50	CCTCCAGTCC ATTCTCTTTG TGCTGCCTAA CGGTCAAGGCC CACAAGCCCT CGGGCGCG	960
	TGTGCCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCATG CACTGGACCT GGTACCTCGC	1020
55	CACCATGTTC CTGTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTT TGTTGTGCA	1080
	GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCCACAACG GTATGCCTGT	1140
60	GATCTCGAAG GAGGAGGCCG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGTCG	1200
	TGATGTCCAC CCGGGTCTAT TTGCCAACTG GTTCACGGGT GGATTGAACT ATCAGATCGA	1260
65	GCACCACTTG TTCCCTTCGA TGCCTCGCCA CAACTTTCA AAGATCCAGC CTGCTGTGCA	1320
	GACCCGTGCA AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGAAACTGC	1380
70	AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA	1440
	GTAAAAAAAAA AAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCTGTGCA CTGCTTCCCT	1500
75	TGTCAAGTCG AGCGTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCTTTTAC	1560

CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAAACAACT TGTTCCCCCC TTCACCG 1617

5

(2) INFORMATION FOR SEQ ID NO:2:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu			
1	5	10	15	
	Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe			
25	20	25	30	
	Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro			
30	35	40	45	
	Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly			
35	50	55	60	
	Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu			
40	65	70	75	80
	Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys			
45	85	90	95	
	Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln			
50	100	105	110	
	Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val			
55	115	120	125	
	Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys			
60	130	135	140	
	Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu			
65	145	150	155	160
	Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His			
70	165	170	175	
	His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe			
75	180	185	190	
	Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys			
80	195	200	205	
	His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp			
85	210	215	220	

	Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met			
	225	230	235	240
5	Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe			
	245	250	255	
	Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala			
	260	265	270	
10	Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly			
	275	280	285	
	Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu			
15	290	295	300	
	Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe			
	305	310	315	320
20	Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser			
	325	330	335	
	Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His			
	340	345	350	
25	Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe			
	355	360	365	
	Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe			
30	370	375	380	
	Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu			
	385	390	395	400
35	Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val			
	405	410	415	
	Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met			
	420	425	430	
40	Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys			
	435	440	445	
	Ala Ala Ser Lys Met Gly Lys Ala Gln			
45	450	455		
	(2) INFORMATION FOR SEQ ID NO:3:			
	(i) SEQUENCE CHARACTERISTICS:			
50	(A) LENGTH: 1488 base pairs			
	(B) TYPE: nucleic acid			
	(C) STRANDEDNESS: single			
	(D) TOPOLOGY: linear			
55	(ii) MOLECULE TYPE: DNA (genomic)			
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:			

60 GTCCCCCTGTC GCTGTCGGCA CACCCCATCC TCCCTCGCTC CCTCTGCGTT TGTCCTTGGC 60

	CCACCGTCTC TCCTCCACCC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAAATAC	120
	ACGATTCTT TTTACTCAGC ACCAACTCAA AATCCTCAAC CGCAACCCIT TTTCAGGATG	180
5	GCACCTCCCA ACACATATCGA TGCCGGTTTG ACCCAGCGTC ATATCAGCAC CTCGGCCCCA	240
	AACTCGGCCA AGCCTGCCCT CGAGCGAAC TACCAGCTCC CCGAGTTCAC CATCAAGGAG	300
10	ATCCGAGAGT GCATCCCTGC CCACTGCTTT GAGCGCTCCG GTCTCCGTGG TCTCTGCCAC	360
	GTTGCCATCG ATCTGACTTG GGCGTCGCTC TTGTTCTGG CTGCGACCCA GATCGACAAG	420
	TTTGAGAATC CCTTGATCCG CTATTTGGCC TGGCCTGTT ACTGGATCAT GCAGGGTATT	480
15	GTCTGCACCG GTGCTGGGT GCTGGCTCAC GAGTGTGGTC ATCAGTCCTT CTCGACCTCC	540
	AAGACCCCTCA ACAACACAGT TGGTTGGATC TTGCACTCGA TGCTCTTGGT CCCCTACCAC	600
20	TCCTGGAGAA TCTCGCACTC GAAGCACCAC AAGGCCACTG GCCATATGAC CAAGGACAG	660
	GTCTTTGTGC CCAAGACCCG CTCCCAGGGT GGCTTCCTC CCAAGGAGAA CGCTGCTGCT	720
	GCCGTTCAAGG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG	780
25	TTCTGGATGG TGATCCAGTT CTTGTTCGGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT	840
	GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC	900
30	CGCAACTTT TCGACATTAT TATCTCGGAC CTGGGTGTGT TGGCTGCCCT CGGTGCCCTG	960
	ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTACCA AGTACTATAT TGTCCCTAC	1020
	CTCTTTGTCA ACTTTGGTT GGTCTGATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG	1080
35	CCCAATTACC GCGAGGGTGC CTGGAATTTC CAGCGTGGAG CTCTTGCAC CGTTGACCGC	1140
	TCGTTGGCA AGTTCTTGGGA CCATATGTTT CACGGCATTG TCCACACCCA TGTGGCCCAT	1200
40	CACTTGTCT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA	1260
	CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCCGATCG TCGTTGCGGT CTGGAGGTCG	1320
	TTCCGTGAGT GCCGATTCTGT GGAGGATCAG GGAGACGTGG TCTTTTCAA GAAGTAAAAA	1380
45	AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC	1440
	CACTTCATAA AAGAACATGA GCTCTAGAGG CGTGTCAATTG GCGCCTCC	1488

50 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile			
	1	5	10	15
5	Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr			
	20	25	30	
	Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala			
10	35	40	45	
	His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile			
	50	55	60	
15	Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp			
	65	70	75	80
	Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp			
	85	90	95	
20	Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu			
	100	105	110	
	Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val			
25	115	120	125	
	Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg			
	130	135	140	
30	Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp			
	145	150	155	160
	Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys			
	165	170	175	
35	Glu Asn Ala Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu			
	180	185	190	
	Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe			
40	195	200	205	
	Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp			
	210	215	220	
45	Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu			
	225	230	235	240
	Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala			
	245	250	255	
50	Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr			
	260	265	270	
	Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu			
55	275	280	285	
	Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr			
	290	295	300	
60	Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp			
	305	310	315	320

	Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
	325 330 335
5	Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
	340 345 350
	Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
	355 360 365
10	Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
	370 375 380
	Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
15	385 390 395

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTTCCTCCA GTTCATCCTC CATTTCGCCA CCTGCATTCT TTACGACCGT TAAGCAAGAT	60
GGGAACGGAC CAAGGAAAAA CCTTCACCTG GGAAGAGCTG GCGGCCCATATA ACACCAAGGA	120
35 CGACCTACTC TTGGCCATCC GCGGCAGGGT GTACGATGTC ACAAAAGTTCT TGAGCCGCCA	180
TCCTGGTGGGA GTGGACACTC TCCTGCTCGG AGCTGCCGA GATGTTACTC CGGTCTTGAA	240
40 GATGTATCAC GCGTTGGGG CTGCAGATGC CATTATGAAG AAGTACTATG TCGGTACACT	300
GGTCTCGAAT GAGCTGCCA TCTTCCCGGA GCCAACGGTG TTCCACAAAA CCATCAAGAC	360
GAGAGTCGAG GGCTACTTTA CGGATCGGAA CATTGATCCC AAGAATAGAC CAGAGATCTG	420
45 GGGACGATAC GCTCTTATCT TTGGATCCTT GATCGCTTCC TACTACGCGC AGCTCTTGT	480
GCCTTCGTT GTCGAACGCA CATGGCTTCA GGTGGTGTGTT GCAATCATCA TGGGATTGCG	540
50 GTGCGCACAA GTCGGACTCA ACCCTCTTCA TGATGCGTCT CACTTTCAAG TGACCCACAA	600
CCCCACTGTC TGGAAAGATTC TGGGAGCCAC GCACGACTTT TTCAACGGAG CATCGTACCT	660
GGTGTGGATG TACCAACATA TGCTCGGCCA TCACCCCTAC ACCAACATTG CTGGAGCAGA	720
55 TCCCGACGTG TCGACGTCTG AGCCCGATGT TCGTCGTATC AAGCCCCAAC AAAAGTGGTT	780
TGTCAACCAC ATCAACCAGC ACATGTTGT TCCTTCCTG TACGGACTGC TGGCGTTCAA	840
60 GGTGCGCATT CAGGACATCA ACATTTGTAA CTTTGTCAAG ACCAACATGACG CTATTCGTGT	900
CAATCCCATC TCGACATGGC ACACGTGAT GTTCTGGGGC GGCAAGGCTT TCTTTGTCTG	960

GTATCGCCTG ATTGTTCCCC TGCAGTATCT GCCCCTGGC AAGGTGCTGC TCTTGTCAC 1020
 GGTGCGGAC ATGGTGTGCGT CTTACTGGCT GGCGCTGACC TTCCAGGCGA ACCACGTTGT 1080
 5 TGAGGAAGTT CAGTGGCCGT TGCCTGACGA GAACGGGATC ATCCAAAAGG ACTGGGCAGC 1140
 TATGCAGGTC GAGACTACGC AGGATTACGC ACACGATTCTG CACCTCTGGA CCAGCATCAC 1200
 10 TGGCAGCTTG AACTACCAGG CTGTGCACCA TCTGTTCCCC AACGTGTCGC AGCACCATTA 1260
 TCCCGATATT CTGGCCATCA TCAAGAACAC CTGCAGCGAG TACAAGGTTC CATAACTTGT 1320
 CAAGGATACG TTTGGCAAG CATTGCTTC ACATTGGAG CACTTGCCTG TTCTTGGACT 1380
 15 CCGTCCCAAG GAAGAGTAGA AGAAAAAAAG CGCCGAATGA AGTATTGCC CTTTTTCTC 1440
 CAAGAATGGC AAAAGGAGAT CAAGTGGACA TTCTCTATGA AGA 1483

20 (2) INFORMATION FOR SEQ ID NO:6:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
- 30 (ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Thr	Asp	Gln	Gly	Lys	Thr	Phe	Thr	Trp	Glu	Glu	Leu	Ala	Ala
1										10					15

His	Asn	Thr	Lys	Asp	Asp	Leu	Leu	Leu	Ala	Ile	Arg	Gly	Arg	Val	Tyr
						20				25					30

Asp	Val	Thr	Lys	Phe	Leu	Ser	Arg	His	Pro	Gly	Gly	Val	Asp	Thr	Leu
					35			40				45			

Leu	Leu	Gly	Ala	Gly	Arg	Asp	Val	Thr	Pro	Val	Phe	Glu	Met	Tyr	His
					50			55				60			

Ala	Phe	Gly	Ala	Ala	Asp	Ala	Ile	Met	Lys	Lys	Tyr	Tyr	Val	Gly	Thr
					65			70			75				80

Leu	Val	Ser	Asn	Glu	Leu	Pro	Ile	Phe	Pro	Glu	Pro	Thr	Val	Phe	His
					85			90				95			

Lys	Thr	Ile	Lys	Thr	Arg	Val	Glu	Gly	Tyr	Phe	Thr	Asp	Arg	Asn	Ile
					100			105				110			

Asp	Pro	Lys	Asn	Arg	Pro	Glu	Ile	Trp	Gly	Arg	Tyr	Ala	Leu	Ile	Phe
					115			120			125				

Gly	Ser	Leu	Ile	Ala	Ser	Tyr	Tyr	Ala	Gln	Leu	Phe	Val	Pro	Phe	Val
					130			135			140				

Val	Glu	Arg	Thr	Trp	Leu	Gln	Val	Val	Phe	Ala	Ile	Ile	Met	Gly	Phe
					145			150			155				160

	Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe			
	165	170	175	
5	Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His			
	180	185	190	
	Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Gln His Met			
10	195	200	205	
	Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val			
	210	215	220	
15	Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp			
	225	230	235	240
	Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly			
	245	250	255	
20	Leu Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe			
	260	265	270	
	Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His			
25	275	280	285	
	Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu			
	290	295	300	
30	Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Phe			
	305	310	315	320
	Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln			
	325	330	335	
35	Ala Asn His Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn			
	340	345	350	
	Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln			
40	355	360	365	
	Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu			
	370	375	380	
45	Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His			
	385	390	395	400
	Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys			
	405	410	415	
50	Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His			
	420	425	430	
	Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu			
55	435	440	445	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10	Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp 1 5 10 15
	Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile 20 25 30
15	Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr 35 40 45
20	Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln 50 55 60
25	Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp 65 70 75 80
30	Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln 85 90 95
35	Gly Phe Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala 100 105 110
40	Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu 115 120 125
45	Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp 130 135 140
50	Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr 145 150 155 160
55	Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu 165 170 175
60	Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser 180 185 190
65	Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met 195 200 205
70	His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro 210 215 220
75	Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn 225 230 235 240
80	Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile 245 250 255
85	Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile 260 265 270
90	Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly 275 280 285

Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
 290 295 300

5 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
 305 310 315 320

Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
 325 330 335

10 Val Phe Ser Arg Leu Asn Glu Val Ser Lys Ala Ala Ser Lys Met Gly
 340 345 350

Lys Ala Gln
 355

15 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
 1 5 10 15

35 Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
 20 25 30

Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
 35 40 45

40 Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
 50 55 60

45 Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
 65 70 75 80

Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
 85 90 95

50 Gly Pro Asn Leu Gln His Ile Pro
 100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

60 (iii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5 Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
 1 5 10 15

10 Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
 20 25 30

15 Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
 35 40 45

20 Arg Phe Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ser Ile
 50 55 60

25 Ala Trp Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser
 65 70 75 80

30 Leu Asp Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser
 85 90 95

35 Thr Lys Phe Phe Ser Ser Leu Thr Ser Arg Phe Tyr Asp Arg Lys Leu
 100 105 110

40 Thr Phe Gly Pro Val Ala Arg Phe Leu Val Ser Tyr Gln His Phe Thr
 115 120 125

45 Tyr Tyr Pro Val Asn Cys Phe Gly Arg Ile Asn Leu Phe Ile Gln Thr
 130 135 140

50 Phe Leu Leu Phe Ser Lys Arg Glu Val Pro Asp Arg Ala Leu Asn
 145 150 155 160

55 Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro Leu Leu Val Ser
 165 170 175

60 Cys Leu Pro Asn Trp Pro Glu Arg Phe Phe Phe Val Phe Thr Ser Phe
 180 185 190

65 Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu Asn His Phe Ala
 195 200 205

70 Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp Trp Phe Glu Lys
 210 215 220

75 Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser Tyr Met Asp Trp
 225 230 235 240

80 Phe Phe Gly Gly Leu Gln Phe Gln Leu Glu His His
 245 250

(2) INFORMATION FOR SEQ ID NO:10:

- 85 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
- 90 (ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 Gly Xaa Xaa Asn Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro
 1 5 10 15
 10 · Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
 20 25 30
 15 Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
 35 40 45
 20 Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
 50 55 60
 25 Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 30 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 35 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 100 105 110
 40 Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

30 (2) INFORMATION FOR SEQ ID NO:11:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: peptide

His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110

5 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125

Lys Pro Leu
 130

10 (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25 Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
 1 5 10 15

Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 20 25 30

30 Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
 35 35 40 45

35 Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
 50 55 60

Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
 65 70 75 80

40 Leu Val Gln Ala Lys Ala Ala
 85

45 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

60 Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val
 1 5 10 15

Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
 20 25 30

Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
 35 40 45

5 Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
 50 55 60

10 Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
 65 70 75 80

15 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
 85 90 95

20 Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
 100 105 110

His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
 115 120 125

25 Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
 130 135 140

(2) INFORMATION FOR SEQ ID NO:14:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 Leu His His Thr Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val Ser
 1 5 10 15

45 Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp Phe
 20 25 30

50 Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly Leu
 35 40 45

55 Leu Ala Phe Lys Val Arg Ile Gln Asp Ile Asn Ile Leu Tyr Phe Val
 50 55 60

60 Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His Thr
 65 70 75 80

65 Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu Ile
 85 90 95

70 Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Phe Thr
 100 105 110

75 Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln Ala
 115 120 125

Asn Tyr Val Val Glu Glu Val Gln Trp Pro Leu Pro Asp Glu Asn Gly
 130 135 140

5 Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln Asp
 145 150 155 160

Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu Asn
 165 170 175

10 Tyr Gln Xaa Val His His Leu Phe Pro His
 180 185

(2) INFORMATION FOR SEQ ID NO:15:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Xaa Xaa His His
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Ala Gln Ile Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn
 1 5 10 15

50 His Asp Lys Pro Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr
 20 25 30

Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu
 35 40 45

55 Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His
 50 55 60

60 Pro Ala Ser Thr Trp Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr
 65 70 75 80

Leu Lys Asp Tyr Ser Val Ser Glu Val Ser Lys Val Tyr Arg Lys Leu
 85 90 95

	Val Phe Glu Phe Ser Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile			
	100	105	110	
5	Met Phe Ala Thr Leu Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val			
	115	120	125	
	Tyr Gly Val Leu Phe Cys Glu Gly Val Leu Val His Leu Phe Ser Gly			
10	130	135	140	
	Cys Leu Met Gly Phe Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp			
	145	150	155	160
15	Ala Gly His Tyr Met Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met			
	165	170	175	
	Gly Ile Phe Ala Ala Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp			
	180	185	190	
20	Lys Trp Asn His Asn Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr			
	195	200	205	
	Asp Pro Asp Leu Gln Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe			
25	210	215	220	
	Phe Gly Ser Leu Thr Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp			
	225	230	235	240
30	Ser Leu Ser Arg Phe Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro			
	245	250	255	
	Ile Met Cys Ala Ala Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met			
	260	265	270	
35	Leu Leu Thr Lys Arg Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly			
	275	280	285	
	Cys Leu Val Phe Ser Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro			
40	290	295	300	
	Asn Trp Gly Glu Arg Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr			
	305	310	315	320
45	Gly Met Gln Gln Val Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val			
	325	330	335	
	Tyr Val Gly Lys Pro Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp			
	340	345	350	
50	Gly Thr Leu Asp Ile Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly			
	355	360	365	
	Gly Leu Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg			
55	370	375	380	
	Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys			
	385	390	395	400
60	His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met			
	405	410	415	

Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr
420 425 430

5 Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr
435 440 445

(2) INFORMATION FOR SEQ ID NO:17:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Leu Thr Ala Glu Arg Ile Lys Phe Thr Gln Lys Arg Gly Phe Arg
1          5           10          15

```

25 Arg Val Leu Asn Gln Arg Val Asp Ala Tyr Phe Ala Glu His Gly Leu
20 25 30

Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu Lys Thr Leu Ile Ile Val
35 40 45

Leu Trp Leu Phe Ser Ala Trp Ala Phe Val Leu Phe Ala Pro Val Ile
50 55 60

35 Phe Pro Val Arg Leu Leu Gly Cys Met Val Leu Ala Ile Ala Leu Ala
65 70 75 80

Ala Phe Ser Phe Asn Val Gly His Asp Ala Asn His Asn Ala Tyr Ser
85 90 95

40 Ser Asn Pro His Ile Asn Arg Val Leu Gly Met Thr Tyr Asp Phe Val
100 105 110

Gly Leu Ser Ser Phe Leu Trp Arg Tyr Arg His Asn Tyr Leu His His
 115 120 125

Thr Tyr Thr Asn Ile Leu Gly His Asp Val Glu Ile His Gly Asp Gly
130 135 140

50 Ala Val Arg Met Ser Pro Glu Gln Glu His Val Gly Ile Tyr Arg Phe
145 150 155 160

Gln Gln Phe Tyr Ile Trp Gly Leu Tyr Leu Phe Ile Pro Phe Tyr Trp
165 170 175

55 The Leu Tyr Asp Val Tyr Leu Val Leu Asn Lys Gly Lys Tyr His Asp
 180 185 190

His Lys Ile Pro Pro Phe Gln Pro Leu Glu Leu Ala Ser Leu Leu Gly
195 200 205

Ile Lys Leu Leu Trp Leu Gly Tyr Val Phe Gly Leu Pro Leu Ala Leu
210 215 220

Gly Phe Ser Ile Pro Glu Val Leu Ile Gly Ala Ser Val Thr Tyr Met
 225 230 235 240
 5 Thr Tyr Gly Ile Val Val Cys Thr Ile Phe Met Leu Ala His Val Leu
 245 250 255
 Glu Ser Thr Glu Phe Leu Thr Pro Asp Gly Glu Ser Gly Ala Ile Asp
 10 260 265 270
 Asp Glu Trp Ala Ile Cys Gln Ile Arg Thr Thr Ala Asn Phe Ala Thr
 275 280 285
 15 Asn Asn Pro Phe Trp Asn Trp Phe Cys Gly Gly Leu Asn His Gln Val
 290 295 300
 Thr His His Leu Phe Pro Asn Ile Cys His Ile His Tyr Pro Gln Leu
 305 310 315 320
 20 Glu Asn Ile Ile Lys Asp Val Cys Gln Glu Phe Gly Val Glu Tyr Lys
 325 330 335
 Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala Ser Asn Tyr Arg Trp Leu
 25 340 345 350
 Glu Ala Met Gly Lys Ala Ser
 355

30 (2) INFORMATION FOR SEQ ID NO:18:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45 Met Thr Ser Thr Thr Ser Lys Val Thr Phe Gly Lys Ser Ile Gly Phe
 1 5 10 15
 Arg Lys Glu Leu Asn Arg Arg Val Asn Ala Tyr Leu Glu Ala Glu Asn
 50 20 25 30
 Ile Ser Pro Arg Asp Asn Pro Pro Met Tyr Leu Lys Thr Ala Ile Ile
 35 40 45
 Leu Ala Trp Val Val Ser Ala Trp Thr Phe Val Val Phe Gly Pro Asp
 55 50 55 60
 Val Leu Trp Met Lys Leu Leu Gly Cys Ile Val Leu Gly Phe Gly Val
 60 65 70 75 80
 Ser Ala Val Gly Phe Asn Ile Ser His Asp Gly Asn His Gly Gly Tyr
 65 85 90 95

	Ser Lys Tyr Gln Trp Val Asn Tyr Leu Ser Gly Leu Thr His Asp Ala			
	100	105	110	
5	Ile Gly Val Ser Ser Tyr Leu Trp Lys Phe Arg His Asn Val Leu His			
	115	120	125	
	His Thr Tyr Thr Asn Ile Leu Gly His Asp Val Glu Ile His Gly Asp			
	130	135	140	
10	Glu Leu Val Arg Met Ser Pro Ser Met Glu Tyr Arg Trp Tyr His Arg			
	145	150	155	160
	Tyr Gln His Trp Phe Ile Trp Phe Val Tyr Pro Phe Ile Pro Tyr Tyr			
15	165	170	175	
	Trp Ser Ile Ala Asp Val Gln Thr Met Leu Phe Lys Arg Gln Tyr His			
	180	185	190	
20	Asp His Glu Ile Pro Ser Pro Thr Trp Val Asp Ile Ala Thr Leu Leu			
	195	200	205	
	Ala Phe Lys Ala Phe Gly Val Ala Val Phe Leu Ile Ile Pro Ile Ala			
	210	215	220	
25	Val Gly Tyr Ser Pro Leu Glu Ala Val Ile Gly Ala Ser Ile Val Tyr			
	225	230	235	240
	Met Thr His Gly Leu Val Ala Cys Val Val Phe Met Leu Ala His Val			
30	245	250	255	
	Ile Glu Pro Ala Glu Phe Leu Asp Pro Asp Asn Leu His Ile Asp Asp			
	260	265	270	
35	Glu Trp Ala Ile Ala Gln Val Lys Thr Thr Val Asp Phe Ala Pro Asn			
	275	280	285	
	Asn Thr Ile Ile Asn Trp Tyr Val Gly Gly Leu Asn Tyr Gln Thr Val			
	290	295	300	
40	His His Leu Phe Pro His Ile Cys His Ile His Tyr Pro Lys Ile Ala			
	305	310	315	320
	Pro Ile Leu Ala Glu Val Cys Glu Glu Phe Gly Val Asn Tyr Ala Val			
45	325	330	335	
	His Gln Thr Phe Phe Gly Ala Leu Ala Ala Asn Tyr Ser Trp Leu Lys			
	340	345	350	
50	Lys Met Ser Ile Asn Pro Glu Thr Lys Ala Ile Glu Gln			
	355	360	365	

(2) INFORMATION FOR SEQ ID NO:19:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 CCAAGCTTCT GCAGGAGCTC TTTTTTTT TTTTT

35

(2) INFORMATION FOR SEQ ID NO:20:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic oligonucleotide"

20 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 21
(D) OTHER INFORMATION: /number= 1
/note= "N=Inosine or Cytosine"

25 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 27
(D) OTHER INFORMATION: /number= 2
/note= "N=Inosine or Cytosine"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35 CUACUACUAC UACAYCAYAC NTAYACNAAY AT

32

(2) INFORMATION FOR SEQ ID NO:21:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Synthetic oligonucleotide"

50 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 13
(D) OTHER INFORMATION: /number= 1
/note= "N=Inosine or Cytosine"

55 (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 19
(D) OTHER INFORMATION: /number= 2
/note= "N=Inosine or Cytosine"

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAUCAUCAUC AUNGGRAANA RRTGRTG

27

(2) INFORMATION FOR SEQ ID NO:22:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
10 (ii) MOLECULE TYPE: other nucleic acid

15 (xii) SEQUENCE DESCRIPTION: SEQ ID NO:22:
CUACUACUAC UAGGAGTCCT CTACGGTGT TTG

33

20 (2) INFORMATION FOR SEQ ID NO:23:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid

30 (xiii) SEQUENCE DESCRIPTION: SEQ ID NO:23:
35 CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG

33

(2) INFORMATION FOR SEQ ID NO:24:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
45 (ii) MOLECULE TYPE: peptide

50 (xiv) SEQUENCE DESCRIPTION: SEQ ID NO:24:
Gln Xaa Xaa His His
1 5

55 (2) INFORMATION FOR SEQ ID NO:25:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CUACUACUAC UACTCGAGCA AGATGGGAAC GGACCAAGG

39

10

(2) INFORMATION FOR SEQ ID NO:26:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: other nucleic acid

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

25

CAUCAUCAUC AUACTCGAGCT ACTCTTCCTT GGGACGGAG

39

(2) INFORMATION FOR SEQ ID NO:27:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: other nucleic acid

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CUACUACUAC UATCTAGACT CGAGACCATT GCTGCTGCTC CAGTGTG

47

45

(2) INFORMATION FOR SEQ ID NO:28:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: other nucleic acid

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

60

CAUCAUCAUC AUAGGCCTCG AGTTACTGCG CCTTACCCAT

40

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

15 CUACUACUA CUAGGATCCA TGGCACCTCC CAACACT

37

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

30 CAUCAUCAU CAUGGTACCT CGAGTTACTT CTTGAAAAAAG AC

42

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 1219 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

	GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA	60
50	ACCTGATCCC AATTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT	120
	TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCAATTG GGGGCCTATG CGTTTGGCAG	180
55	TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCCACAAATG CTGCCTTGG	240
	CAACTGCAAA GCAATGTGGA ATCGCTGGTT TGGAATGTTT GCTAACCTTC CTATTGGGAT	300
	TCCATATTCA ATTCCTTTA AGAGGTATCA CATGGATCAT CATCGGTACC TTGGAGCTGA	360
60	TGGCGTCGAT GTAGATATTC CTACCGATTT TGAGGGCTGG TTCTTCTGTA CCGCTTCAG	420
	AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTATGCC TTTCGACCTC TGTTCATCAA	480

	CCCCAAACCA ATTACGTATC TGGAAGTTAT CAATACCGTG GCACAGGTCA CTTTGACAT	540
5	TTTAATTAT TACTTTTGG GAATTAAATC CTTAGTCTAC ATGTTGGCAG CATCTTACT	600
	TGGCCTGGGT TTGCACCAA TTTCTGGACA TTTTATAGCT GAGCATTACA TGTTCTAAA	660
	GGGTCAATGAA ACTTACTCAT ATTATGGCC TCTGAATTAA CTTACCTTCA ATGTGGGTTA	720
10	TCATAATGAA CATCATGATT TCCCCAACAT TCCTGGAAAA AGTCTTCCAC TGGTGAGGAA	780
	AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAAT TCCTGGATAA AAGTACTGTA	840
15	TGATTTGTG ATGGATGATA CAATAAGTCC CTACTCAAGA ATGAAGAGGC ACCAAAAAGG	900
	AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AAACTTAGA	960
	TGATAAAATG GAATTTTGC ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCT	1020
20	GGCACAAATT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTTAAACAGT	1080
	CAGCCTGACT CTGTAUTGCT CAGTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG	1140
25	TCATTGAGGA TGTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTAA AAAAGCTTCT	1200
	AAAAAGCTAT TTCGCCAGG	1219

(2) INFORMATION FOR SEQ ID NO:32:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 655 base pairs
	(B) TYPE: nucleic acid
35	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

45	TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT	60
	GGGCCTTTTC TTCATAGTCA GGTCCTGGA AAGCACTGG TTTGTGTGGG TGACACAGAT	120
	GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT	180
50	CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGTTTCAGTG GACACCTCAA	240
	CTTCCAGATT GAGCACCATC TTTTCCCAC GATGCCCTCGA CACAATTACC ACAAAAGTGGC	300
55	TCCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCAAGTCCA AGCCCCTGCT	360
	GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC	420
	CTATCTTCAC CAATAACAAC AGCCACCCCTG CCCAGTCTGG AAGAAGAGGA GGAAGACTCT	480
60	GGAGCCAAGG CAGAGGGAG CTTGAGGGAC AATGCCACTA TAGTTAATA CTCAGAGGGG	540
	GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTATCT TCTAGCCACA	600

GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

5 (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTCTTTACT TTGGCAATGG CTGGATT CCT ACCCTCATCA CGGCCTTG CTTGCTACC	60
TCTCAGGCC AAGCTGGATG GCTGAAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA	120
CCCAGTGG ACCACCTTGT CCACAAATT GTCATTGCC ACTTAAAGGG TGCCCTGCC	180
AACTGGTGG ATCATGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT	240
25 CCCGATGTGA ACATGCTGCA CGTGTGTT CTGGCGAAT GGCAAGCCAT CGAGTACGGC	300
AAGA	304

30 (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAGGGACCTA CCCCGCGCTA CTTCACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCAG	60
GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CGGCCGGCAT	120
45 CCAGGGGGCT CCCGGGTCA CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTGTG	180
GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA	240
50 CTGTCTCCAG AGCAGCCCAG CTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTC	300
CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTCTTC	360
55 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTGGGTC	420
TTTGGGACGT CCTTTTGCC CTTCCCTCCTC TGTGCGGTGC TGCTCAGTGC AGTCAGGCC	480
CAGGCTGGCT GGCTGCAGCA TGACTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG	540
60 AACCATCTGC TACATCATT TGATGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG	600
AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC	660

	AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG	720
5	AAGAAAAAAAT ATATGCCGTA CAACCACCAAG CACARATACT TCTTCCTAAT TGGGCCCCA	780
	GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG	840
	TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC	900
10	ACCGCAAATG CTTCTAAA	918

(2) INFORMATION FOR SEQ ID NO:35:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1686 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
25	GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA	60
	AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGCG	120
30	AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAAGC	180
	ACGAATACTT CTTCCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTC CAGTACCAGA	240
35	TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT	300
	ACATCCGGTT CTTCATCACCC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTCC	360
	TCAACTTCAT CAGGTTCTG GAGAGCCACT GGTTTGTGTG GGTACACACAG ATGAATCACA	420
40	TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA	480
	CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGACACACCTT AACTTCCAGA	540
45	TTGAGCACCA CCTCTTCCCC ACCATGCCCG GGCACAACCTT ACACAAAGATC GCCCCGCTGG	600
	TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC	660
	TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC	720
50	ACAAATGAAG CCACAGCCCC CGGGACACCCG TGGGGAAAGGG GTGCAGGTGG GGTGATGGCC	780
	AGAGGAATGA TGGGCTTTG TTCTGAGGGG TGTCCGAGAG GCTGGTGTAT GCACTGCTCA	840
55	CGGACCCCAT GTTGGATCTT TCTCCCTTTC TCCTCTCCTT TTTCTCTCA CATCTCCCC	900
	ATAGCACCCCT GCCCTCATGG GACCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC	960
	TCCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC	1020
60	TGTCTTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGGAGA CCAGCGGTCC ATGGGTCTGG	1080
	CCTGTGAGTC TCCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCGCTTTG GTTCTTCAGA	1140

	TGCTCTTGGG GTTCATAGGG GCAGGTCTA GTCGGGCAGG GCCCCTGACC CTCCCGGCCT	1200
5	GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCCTT CATAGAGAGG CCTGCTTGT	1260
	TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTAAAGTAC CCGAGGCCTC TCTTAAGATG	1320
	TCCAGGGCCC CAGGCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC	1380
10	CACCCCCATCA CTAGAGTGCT CTGACCCCTGG GCTTCACGG GCCCCATTCC ACCGCCTCCC	1440
	CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGACTCAGCA	1500
15	GAGGCAGTGG CCACGTTCAAG GGAGGGGCCG GCTGGCCCTGG AGGCTCAGCC CACCCCTCCAG	1560
	CTTTTCCTCA GGGTGTCTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCCT TCTCCAAGG	1620
	CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG	1680
20	GCCCTG	1686

(2) INFORMATION FOR SEQ ID NO:36:

- | | |
|----|--|
| 25 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 1843 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: single |
| 30 | (D) TOPOLOGY: linear |
| | (ii) MOLECULE TYPE: other nucleic acid (Contig 2535) |
| 35 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36: |

35	GTCTTTTACT TTGGCAATGG CTGGATTCCCT ACCCTCATCA CGGCCTTGT CCTTGCTACC	60
	TCTCAGGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA	120
40	CCCAAGTGGA ACCACCTTGT CCACAAATTG GTCATTGGCC ACTTAAAGGG TGCCTCTGCC	180
	AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT	240
45	CCCGATGTGA ACATGCTGCA CGTGTGTTCTGGCAAT GGCAAGCCCAT CGAGTACGGC	300
	AAGAAGAACG TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG	360
	CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT	420
50	AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC	480
	ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTCCTCA ACTTCATCAG GTTCCTGGAG	540
55	AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG	600
	GCCTACCGTG ACTGGTTCAAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC	660
	TTCAACGACT GGTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC	720
60	ATGCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT	780
	GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG	840

	AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCGG	900
5	GACACCGTGG GGAAGGGGTG CAGGTGGGT GATGGCCAGA GGAATGATGG GCTTTGTT	960
	TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCCATGTT GGATCTTCT	1020
	CCCTTCTCC TCTCCTTTT CTCTTCACAT CTCCCCATA GCACCCCTGCC CTCATGGAC	1080
10	CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCCCTC	1140
	TTCCAAGGAG CAGAGAGGTG GCCACCGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCC	1200
15	CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CCTTGCAGCC	1260
	TGGTCACTAG GCATCACCCCC CGCTTGGTT CTTCAGATGC TCTTGGGTT CATAGGGCA	1320
	GGTCCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG	1380
20	CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTTAC AAAGCTCGGG TCTCCCTCCT	1440
	GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCCGGGGC	1500
25	ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG	1560
	ACCCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG	1620
	ACCAAAGGGG GAGTCCCTCG TCTCTTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA	1680
30	GGGGCCGGCT GCCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCCTCAGGG TGTCCGTAGG	1740
	TCCAAGATTC TGGAGCAATC TGACCCCTCT CCAAAGGCTC TGTATCAGC TGGGCAGTGC	1800
35	CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG	1843

(2) INFORMATION FOR SEQ ID NO:37:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2257 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
50	CAGGGACCTA CCCCGCGCTA CTTCACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCAG	60
	GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT	120
	CCAGGGGGCT CCCGGGTCA CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTGTG	180
55	GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA	240
	CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC	300
60	CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTCTTC	360
	CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGTC	420

	TTTGGGACGT CCTTTTGCC CTTCCCTCTC TGTGCGGTGC TGCTCAGTGC AGTCAGCAG	480
	GCCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG	540
5	TGGAACCACC TTGTCCACAA ATTGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACTGG	600
	TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACAA TCTTCCACAA GGATCCCGAT	660
10	GTGAACATGC TGCACGTGTT TGTTCTGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG	720
	AAGCTGAAAT ACCTGCCCTA CAATCACCAAG CACGAATACT TCTTCCTGAT TGGGCCGCCG	780
	CTGCTCATCC CCATGTATTT CCAGTACCAAG ATCATCATGA CCATGATCGT CCATAAGAAC	840
15	TGGGTGGACC TGGCCTGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT	900
	TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTCCCT GGAGAGCCAC	960
20	TGGTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC	1020
	CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC	1080
	GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTCCC CACCATGCC	1140
25	CGGGCACAACT TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT	1200
	GAATACCAGG AGAACCGCCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAC	1260
30	TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC	1320
	GTGGGGAAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG	1380
	GTGTCCGAGA GGCTGGTGTG TGCACTGCTC ACGGACCCCA TGTTGGATCT TTCTCCCTT	1440
35	CTCCTCTCCT TTTCTCTTC ACATCTCCC CATAGCACCC TGCCCTCATG GGACCTGCC	1500
	TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCCTAGCCC CTTCTCCAA	1560
40	GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGCTCTACC TCCACTCTCT GCCCCTAAAG	1620
	ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA	1680
	CTAGGCATCA CCCCCGCTT GGTTCTTCAG ATGCTTTGG GGTTCATAGG GGCAGGTCT	1740
45	AGTCGGGCAG GGCCCCGTAC CCTCCCGGCC TGGCTTCACT CTCCCTGACG GCTGCCATTG	1800
	GTCCACCCCT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT	1860
50	CGGTTAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCGC GGGCACAGCC	1920
	AGCCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCTG	1980
	GGCTTTCACG GGCCCCATTC CACCGCCTCC CCAACTTGAG CCTGTGACCT TGGGACCAA	2040
55	GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGCC	2100
	GGCTGGCCTG GAGGCTCAGC CCACCCCTCA GCTTTCTC AGGGTGTCTT GAGGTCCAAG	2160
60	ATTCTGGAGC AATCTGACCC TTCTCCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA	2220
	ATCCCTGGCC ATTTGGCCCC AGGGGACGTG GGCCCTG	2257

(2) INFORMATION FOR SEQ ID NO:38:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

15	His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
	1 5 10 15
	Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
	20 25 30
20	Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
	35 40 45
	Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
	50 55 60
25	Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
	65 70 75
	Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
	80 85 90
	Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
	95 100 105
30	Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
	110 115 120
	Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
	125 130 135
	Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
	140 145 150
35	Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
	155 160 165
	Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile
	170 175 180
40	Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu
	185 190 195
	Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His
	200 205 210
	Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr
	215 220 225
45	Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
	230 235 240
	His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu
	245 250 255
50	Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro
	260 265 270
	His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp
	275 280 285
	Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly
	290 295 300
55	Glu Met Val Leu Glu *** Ile Ser Leu Val Pro Lys Gly Phe Phe
	305 310 315
	Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr *** Thr
	320 325 330
60	*** Asp Gln *** Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser
	335 340 345
	Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe *** Thr Val
	350 355 360

Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu ***
 365 370 375
 Leu Val Tyr Tyr Arg His *** Gly Cys Phe Thr His Val Cys His
 380 385 390
 5 Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala
 400 405 410
 Arg

10 (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

	Tyr	Leu	Leu	Arg	Pro	Leu	Leu	Pro	His	Leu	Cys	Ala	Thr	Ile	Gly
25	1	5				10				15					
	Ala	Glu	Ser	Phe	Leu	Gly	Leu	Phe	Phe	Ile	Val	Arg	Phe	Leu	Glu
		20					25				30				
	Ser	Asn	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Pro	Met
30		35				35		40		45					
	His	Ile	Asp	His	Asp	Arg	Asn	Met	Asp	Trp	Val	Ser	Thr	Gln	Leu
		50				50		55		60					
	Gln	Ala	Thr	Cys	Asn	Val	His	Lys	Ser	Ala	Phe	Asn	Asp	Trp	Phe
35		65				65		70		75					
	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr
		80				80		85		90					
	Met	Pro	Arg	His	Asn	Tyr	His	Lys	Val	Ala	Pro	Leu	Val	Gln	Ser
40		95				95		100		105					
	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Ser	Lys	Pro	Leu	Leu
		110				110		115		120					
	Ser	Ala	Phe	Ala	Asp	Ile	Ile	His	Ser	Leu	Lys	Glu	Ser	Gly	Gln
45		125				125		130		135					
	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Gln	***	Gln	Gln	Pro	Pro	Cys
		140				140		145		150					
	Pro	Val	Trp	Lys	Lys	Arg	Arg	Lys	Thr	Leu	Glu	Pro	Arg	Gln	Arg
50		155				155		160		165					
	Gly	Ala	***	Gly	Thr	Met	Pro	Leu	***	Phe	Asn	Thr	Gln	Arg	Gly
		170				170		175		180					
	Leu	Gly	Leu	Gly	Thr	***	Ser	Leu	***	Leu	Lys	Leu	Leu	Pro	Phe
		185				185		190		195					
	Ile	Phe	***	Pro	Gln	Phe	***	Asp	Pro	Lys	Trp	Gly	Val	Asp	Thr
55		200				200		205		210					
	Glu	Val	Pro	Arg	Arg	Glu	Gly	Ala							
		215													

55 (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5

	Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala		
1	5	10	15
	Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His		
10	20	25	30
	Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His		
	35	40	45
	Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala		
15	50	55	60
	Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn		
	65	70	75
	Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xxx		
	80	85	

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

35

	Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln		
1	5	10	15
	Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val		
	20	25	30
40	Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg		
	35	40	45
	Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val		
	50	55	60
	Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser		
45	65	70	75
	Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro		
	80	85	90
	Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala		
50	95	100	105
	Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe		
	110	115	120
	Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp		
	125	130	135
	Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu		
55	140	145	150
	Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu		
	155	160	165
	Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp		
	170	175	180
60	Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala		
	185	190	195
	Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys		
	200	205	210

Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
 215 220 225
 Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
 230 235 240
 5 Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xxx Tyr Phe Phe
 245 250 255
 Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
 260 265 270
 Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
 10 275 280 285
 Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
 290 295 300
 Thr Ala Asn Ala Ser Lys
 305

15

(2) INFORMATION FOR SEQ ID NO:42:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

30 His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe
 1 5 10 15
 Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val
 20 25 30
 35 Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu
 35 40 45
 Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His
 50 55 60
 Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
 65 70 75
 40 Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp
 80 85 90
 Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile
 95 100 105
 45 Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu
 110 115 120
 Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr
 125 130 135
 Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg
 140 145 150
 50 Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
 155 160 165
 Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile
 170 175 180
 55 Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys
 185 190 195
 Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu
 200 205 210
 Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
 215 220 225
 60 Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His
 230 235 240
 Lys *** Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg

	245	250	255
	Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe *** Gly Val		
	260	265	270
5	Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp		
	275	280	285
	Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His		
	290	295	300
	Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro		
	305	310	315
10	Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly		
	320	325	330
	Ala Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser		
	335	340	345
15	Leu Pro Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala		
	350	355	360
	Cys Glu Ser Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala		
	365	370	375
	Leu Val Leu Gln Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser		
	380	385	390
20	Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu His Ser Pro ***		
	400	405	410
	Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu		
	415	420	425
25	Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly		
	430	435	440
	Leu Ser *** Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser		
	445	450	455
	Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His *** Ser		
	460	465	470
30	Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro		
	475	480	485
	Thr *** Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu		
	490	495	500
35	Leu *** Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly		
	505	510	515
	Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val		
	520	525	530
	Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala		
	535	540	545
40	Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala		
	550	555	560
	Pro Gly Asp Val Gly Pro Xxx		
	565		

45

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

60

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala		
1	5	10
Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His		15

	20	25	30
	Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His		
	35	40	45
5	Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala		
	50	55	60
	Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn		
	65	70	75
	Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val		
	80	85	90
10	Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys		
	95	100	105
	Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly		
	110	115	120
15	Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met		
	125	130	135
	Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val		
	140	145	150
	Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly		
	155	160	165
20	Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu		
	170	175	180
	Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met		
	185	190	195
25	Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu		
	200	205	210
	Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe		
	215	220	225
	Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr		
30	230	235	240
	Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser		
	245	250	255
	Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu		
	260	265	270
35	Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys		
	275	280	285
	Leu Trp Leu Asp Ala Tyr Leu His Lys *** Ser His Ser Pro Arg		
	290	295	300
	Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn		
40	305	310	315
	Asp Gly Leu Leu Phe *** Gly Val Ser Glu Arg Leu Val Tyr Ala		
	320	325	330
	Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe Leu Leu Ser		
	335	340	345
45	Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser Trp Asp		
	350	355	360
	Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro Val		
	365	370	375
	Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly		
50	380	385	390
	Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly		
	400	405	410
	Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala		
	415	420	425
55	Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu		
	430	435	440
	Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu		
	445	450	455
	Pro Ala Trp Leu His Ser Pro *** Arg Leu Pro Leu Val His Pro		
60	460	465	470
	Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro		
	475	480	485
	Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser *** Asp Val Gln Gly		

	490	495	500
	Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys		
	505	510	515
5	Ser Pro Pro Pro His His *** Ser Ala Leu Thr Leu Gly Phe His		
	520	525	530
	Gly Pro His Ser Thr Ala Ser Pro Thr *** Ala Cys Asp Leu Gly		
	535	540	545
	Thr Lys Gly Gly Val Pro Arg Leu Leu *** Leu Ser Arg Gly Ser		
	550	555	560
10	Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His		
	565	570	575
	Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu		
	580	585	590
15	Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys		
	595	600	605
	Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xxx		
	610	615	620

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 757 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

	Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln			
35	1	5	10	15
	Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val			
	20	25	30	
	Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg			
	35	40	45	
40	Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val			
	50	55	60	
	Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser			
	65	70	75	
45	Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro			
	80	85	90	
	Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala			
	95	100	105	
	Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe			
50	110	115	120	
	Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp			
	125	130	135	
	Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu			
	140	145	150	
55	Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp			
	155	160	165	
	Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys			
	170	175	180	
	Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly			
60	185	190	195	
	Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala			
	200	205	210	
	Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His			

	215	220	225
	Val Phe Val Leu Gly Glu Trp Gln Pro Ile	Glu Tyr Gly Lys Lys	
	230	235	240
5	Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln	His Glu Tyr Phe Phe	
	245	250	255
	Leu Ile Gly Pro Pro Leu Leu Ile Pro Met	Tyr Phe Gln Tyr Gln	
	260	265	270
	Ile Ile Met Thr Met Ile Val His Lys Asn	Trp Val Asp Leu Ala	
	275	280	285
10	Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe	Ile Thr Tyr Ile Pro	
	290	295	300
	Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe	Leu Asn Phe Ile Arg	
	305	310	315
15	Phe Leu Glu Ser His Trp Phe Val Trp Val	Thr Gln Met Asn His	
	320	325	330
	Ile Val Met Glu Ile Asp Gln Glu Ala Tyr	Arg Asp Trp Phe Ser	
	335	340	345
	Ser Gln Leu Thr Ala Thr Cys Asn Val Glu	Gln Ser Phe Phe Asn	
	350	355	360
20	Asp Trp Phe Ser Gly His Leu Asn Phe Gln	Ile Glu His His Leu	
	365	370	375
	Phe Pro Thr Met Pro Arg His Asn Leu His	Lys Ile Ala Pro Leu	
	380	385	390
25	Val Lys Ser Leu Cys Ala Lys His Gly Ile	Glu Tyr Gln Glu Lys	
	400	405	410
	Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile	Arg Ser Leu Lys Lys	
	415	420	425
	Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu	His Lys *** Ser His	
	430	435	440
30	Ser Pro Arg Asp Thr Val Gly Lys Gly Cys	Arg Trp Gly Asp Gly	
	445	450	455
	Gln Arg Asn Asp Gly Leu Leu Phe *** Gly	Val Ser Glu Arg Leu	
	460	465	470
35	Val Tyr Ala Leu Leu Thr Asp Pro Met Leu	Asp Leu Ser Pro Phe	
	475	480	485
	Leu Leu Ser Phe Phe Ser Ser His Leu Pro	His Ser Thr Leu Pro	
	490	495	500
	Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln	Pro Ser Ala Met Ala	
40	505	510	515
	Leu Pro Val Pro Pro Ser Pro Phe Phe Gln	Gly Ala Glu Arg Trp	
	520	525	530
	Pro Pro Gly Val Ala Leu Ser Tyr Leu His	Ser Leu Pro Leu Lys	
	535	540	545
45	Met Gly Gly Asp Gln Arg Ser Met Gly Leu	Ala Cys Glu Ser Pro	
	550	555	560
	Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro	Ala Leu Val Leu Gln	
	565	570	575
	Met Leu Leu Gly Phe Ile Gly Ala Gly Pro	Ser Arg Ala Gly Pro	
	580	585	590
50	Leu Thr Leu Pro Ala Trp Leu His Ser Pro	*** Arg Leu Pro Leu	
	595	600	605
	Val His Pro Phe Ile Glu Arg Pro Ala Leu	Leu Gln Ser Ser Gly	
	610	615	620
55	Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg	Gly Leu Ser *** Asp	
	625	630	635
	Val Gln Gly Pro Arg Pro Ala Gly Thr Ala	Ser Pro Asn Leu Gly	
	640	645	650
	Pro Trp Lys Ser Pro Pro Pro His His ***	Ser Ala Leu Thr Leu	
	655	660	665
60	Gly Phe His Gly Pro His Ser Thr Ala Ser	Pro Thr *** Ala Cys	
	670	675	680
	Asp Leu Gly Thr Lys Gly Val Pro Arg Leu	Leu *** Leu Ser	

	685	690	695
	Arg Gly Ser Gly His Val Gln Gly Gly Ala	Gly Trp Pro Gly	Gly
	700	705	710
5	Ser Ala His Pro Pro Ala Phe Pro Gln Gly	Val Leu Arg Ser Lys	
	715	720	725
	Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys	Ala Leu Leu Ser Ala	
	730	735	740
	Gly Gln Cys Gln Pro Ile Pro Gly His Leu	Ala Pro Gly Asp Val	
	745	750	755
10	Gly Pro Xxx		

(2) INFORMATION FOR SEQ ID NO:45:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 746 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: nucleic acid

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

25	CGTATGTCAC TCCATTCCAA ACTCGTTCAT GGTATCATAA ATATCAACAC ATTTACGCTC	60
	CACTCCTCTA TGGTATTAC ACACCTCAAAT ATCGTACTCA AGATTGGAA GCTTTTGTA	120
	AGGATGGTAA AAATGGTGCA ATTCTGTTA GTGTCGCCAC AAATTCGAT AAGGCGCCTT	180
	ACGTCAATTGG TAAATTGTCCT TTGTTTTCTC TCCGTTTCAT CCTTCCACTC CGTTATCATA	240
30	GCTTTACAGA TTTAATTGTT TATTCCTCA TTGCTGAATT CGTCTTGGT TGTTATCTCA	300
	CAATTAATTG CCAAGTTAGT CATGTCGCTG AAGATCTCAA ATTCTTTGCT ACCCTGAAA	360
	GACCAGATGA ACCATCTCAA ATCAATGAAG ATTGGGCAAT CCTTCACCTT AAAACTACTC	420
	AAGATTATGG TCATGGTCA CTCTTTGTA CCTTTTTAG TGTTCTTA AATCATCAAG	480
	TTGTTCATCA TTTATTCCCA TCAATTGCTC AAGATTCTCA CCCACAACTT GTACCAATTG	540
35	TAAAAGAAGT TTGTAAGAA CATAACATTA CTTACCACAT TAAACCAAA TTCACGAAAG	600
	CTATTATGTC ACACATTAAT TACCTTTACA AAATGGGTAA TGATCCAGAT TATGTTAAA	660
	AACCATTAGC CTCAAAAGAT GATTAATGAA AATAACTTAA AAACCAATTA TTTACTTTG	720
	ACAAACAGTA ATATTAATAA ATACAA	746

(2) INFORMATION FOR SEQ ID NO:46:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

	Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln			
	1	5	10	15
	His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr			
55	20	25	30	
	Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly			
	35	40	45	
	Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr			
	50	55	60	
60	Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro			
	65	70	75	
	Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile			
	80	85	90	
65	Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val			
	95	100	105	

Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
 110 115 120
 Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
 125 130 135
 5 Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
 140 145 150
 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
 155 160 165
 10 Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
 170 175 180
 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
 185 190 195
 Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
 200 205 210
 15 Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
 215 220 225
 Asp Asp ***

20 (2) INFORMATION FOR SEQ ID NO 47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 494 nucleic acids
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

30 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:47:

35	TTTTGGAAGG NTCCAAGTTN ACCACGGANT NGGCAAGTTN ACGGGCGGA AANCGGTTTT	60
	CCCCCCAAGC CTTTTGTCTGA CTGGTTCTGT GGTGGCTTC AGTACCAAGT CGACCACAC	120
	TTATTCCTCCA GCCTGCCCG ACACAATCTG GCCAAGACAC ACGCACTGGT CGAATCGTTC	180
	TGCAAGGAGT GGGGTGTCCA GTACCACGAA GCGCACCTCG TGGACGGGAC CATGGAAGTC	240
	TTGCACCAATT TGGGCAGCGT GGCAGCGAA TTCGTCGTGG ATTTTGTACG CGACGGACCC	300
	GCCATGTAAT CGTCGTTCTCGT GACGATGCAA GGGTTCACGC ACATCTACAC ACACTCACTC	360
40	ACACAACCTAG TGTAACCTCGT ATAGAATTG TGTCGACCT GGACCTTGTT TGAATGGTTG	420
	GGGATAGGGT AGGTAGGCGG ACGCGTGGGT CGNCCCCGGG AATTCTGTGA CCGGTACCTG	480
	GCCCCGTNA AAGT	494

45 (2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

60	Phe Trp Lys Xxx Pro Ser Xxx Pro Arg Xxx Xxx Gln Val Xxx Gly	
	1 5 10 15	
	Ala Glu Xxx Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys	
	20 25 30	
	Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu	
	35 40 45	
	Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe	
	50 55 60	
65	Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp	
	65 70 75	

Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
 65 70 75
 Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
 80 85

5

10

(2) INFORMATION FOR SEQ ID NO:49:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 520 nucleic acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGATGGAGTT	CGTCTGGATC	GCTGTGCGCT	ACGCGACGTG	GTTAAAGCGT	CATGGGTGCG	60
CTTGGGTACA	CGCGGGGCA	GTCGTTGGC	ATGTAATTGT	GCCTTGG	TCTCGGCTGC	120
ATTTACATT	TTCTGCAGTT	CGCCGTAAGT	CACACCCATT	TGCCCGTGAG	CAACCCGGAG	180
GATCAGCTGC	ATTGGCTCGA	GTACGCGCGG	ACCACACTGT	GAACATCAGC	ACCAAGTCGT	240
GGTTTGTAC	ATGGTGGATG	TCGAACCTCA	ACTTTCAGAT	CGAGCACAC	CTTTCCCCA	300
CGGCGCCCCA	GTTCGTTTC	AAGGAGATCA	GCCCCGCGGT	CGAGGCCCTC	TTCAAGCGCC	360
30	ACGGTCTCCC	TTACTACGAC	ATGCCCTACA	CGAGCGCCGT	CTCCACCACC	420
ACGGTCTCCC	TTACTACGAC	ATGCCCTACA	CGAGCGCCGT	CTCCACCACC	TTGCCAACC	480
TTAATTCCCC	CGGCCATTCC	GTGCGCGACG	CCAAGCGCGA	CTAGCCTCTT	TTCCCTAGACC	520

35

(2) INFORMATION FOR SEQ ID NO:50:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Glu	Phe	Val	Trp	Ile	Ala	Val	Arg	Tyr	Ala	Thr	Trp	Phe	Lys	
1					5				10				15		
50	Arg	His	Gly	Cys	Ala	Trp	Val	His	Ala	Gly	Ala	Val	Val	Gly	His
									20		25			30	
	Val	Leu	Val	Arg	Leu	Trp	Ser	Arg	Leu	His	Leu	His	Phe	Ser	Ala
									35		40			45	
55	Val	Arg	Arg	Lys	Ser	His	Pro	Phe	Ala	Arg	Glu	Gln	Pro	Gly	Gly
									50		55			60	
	Ser	Ala	Ala	Leu	Ala	Arg	Val	Arg	Ala	Asp	His	Thr	Val	Asn	Ile
									65		70			75	
60	Ser	Thr	Lys	Ser	Trp	Phe	Val	Thr	Trp	Trp	Met	Ser	Asn	Leu	Asn
									80		85			90	
	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Ala	Pro	Gln	Phe	Arg
									95		100			105	
65	Phe	Lys	Glu	Ile	Ser	Pro	Arg	Val	Glu	Ala	Leu	Phe	Lys	Arg	His
									110		115			120	
	Gly	Leu	Pro	Tyr	Tyr	Asp	Met	Pro	Tyr	Thr	Ser	Ala	Val	Ser	Thr
									125		130			135	
	Thr	Phe	Ala	Asn	Leu	Tyr	Ser	Val	Gly	His	Ser	Val	Gly	Asp	Ala

140 145 150
Lys Arg Asp

5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 nucleic acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: nucleic acid

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

20	ACCGCGTCCGC CCACCGTCC GC CGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC	60
	GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCTTTTG	120
	GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC	180
	TCAGGGTCCG TGCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCTA	240
	TTGGCTTGAC GACCAGTTGT GCGAGTTCTT TTACGGCGTT GGTTGTGGCA TGAGCCGTCA	300
25	TTACTGGAAA AACCAAGCACA GCAAACACCA CGCAGCGCCA ACCCGGCTCG AGCACGATGT	360
	AGATCTAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC	420

30 (2) INFORMATION FOR SEQ ID NO:52:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

1	Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly	
5	5 10 15	
45	Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu	
20	20 25 30	
50	Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser	
35	35 40 45	
55	Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser	
50	50 55 60	
60	Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser	
65	65 70 75	
75	Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe	
65	65 70 75	
80	Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln	
80	80 85 90	
95	His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val	
95	95 100 105	
100	Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val	
110	110 115 120	
125	Arg Lys Val Arg Pro	

What is claimed is:

1. A nucleic acid construct comprising:

One or more nucleotide sequences depicted in a SEQ ID NO: selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3 and SEQ ID NO:5,
5 wherein said one or more nucleotide sequences is linked to a heterologous nucleotide sequence.

2. A nucleic acid construct comprising:

One or more nucleotide sequences depicted in a SEQ ID NO: selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3 and SEQ ID NO:5,
10 wherein said one or more nucleotide sequences is operably associated with an expression control sequence functional in a plant cell.

3. The nucleic acid construct according to claim 2, wherein said nucleotide
15 sequence has an average A + T content of less than about 60%.

4. The nucleic acid construct according to claim 2, wherein said nucleotide sequence is derived from a fungus.

20 5. The nucleic acid construct according to claim 4, wherein said fungus is of the genus *Mortierella*.6. The nucleic acid construct according to claim 5, wherein said fungus is of the species *alpina*.

25

7. A nucleic acid construct comprising:

A nucleotide sequence which encodes a polypeptide comprising an amino acid sequence depicted in SEQ ID NO:2, wherein said nucleotide sequence is

operably associated with a transcription or an expression control sequence function in a plant cell, wherein said nucleotide sequence encodes a functionally active polypeptide which desaturates a fatty acid molecule at carbon 6 from the carboxyl end of said fatty acid molecule.

5

8. A nucleic acid construct comprising:

A nucleotide sequence which encodes a polypeptide comprising an amino acid sequence depicted in SEQ ID NO:4, wherein said nucleotide sequence is operably associated with a transcription or an expression control sequence functional in a plant cell, wherein said nucleotide sequence encodes a functionally active polypeptide which desaturates a fatty acid molecule at carbon 12 from the carboxyl end of said fatty acid molecule.

10

9. A nucleic acid construct comprising:

15

A nucleotide sequence which encodes a polypeptide comprising an amino acid sequence depicted in SEQ ID NO:6, wherein said nucleotide sequence is operably associated with a transcription or an expression control sequence function in a plant cell, wherein said nucleotide sequence encodes a functionally active polypeptide which desaturates a fatty acid molecule at carbon 5 from the carboxyl end of said fatty acid molecule.

20

10. A nucleic acid construct comprising:

25

at least one nucleotide sequence which encodes a functionally active desaturase having an amino acid sequence depicted in a SEQ ID NO: selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4 and SEQ ID NO:6, wherein said nucleotide sequence is operably associated with a promoter functional in a plant cell.

11. The nucleic acid construct according to claim 10, wherein said plant cell is a seed cell.
12. The nucleic acid construct according to claim 11, wherein said seed cell is
5 an embryo cell.
13. A recombinant plant cell comprising:

At least one copy of a DNA sequence which encodes at least one functionally active *Mortierella alpina* fatty acid desaturase which results in the
10 production of a polyunsaturated fatty acid, wherein said fatty acid desaturase has an amino acid sequence as depicted in a SEQ ID NO: selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, and SEQ ID NO:6, wherein said cell was transformed with a vector comprising said DNA sequence, and
15 wherein said DNA sequence is operably associated with an expression control sequence.
14. The recombinant plant cell of claim 13, wherein said polyunsaturated fatty acid is selected from the group consisting of LA, ARA, GLA, DGLA, SDA and EPA.
20
15. The recombinant plant cell of claim 13, wherein said recombinant plant cell is enriched in a fatty acid selected from the group consisting of 18:1, 18:2, 18:3 and 18:4.
25
16. The recombinant plant cell of claim 15, wherein said plant cell is selected from the group consisting of *Brassica*, soybean, safflower, corn, flax, and sunflower.

17. The recombinant plant cell according to claim 16, wherein said expression control sequence is endogenous to said plant cell.

18. One or more plant oils expressed by said recombinant plant cell of claim 16.

5

19. A method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of:

growing a plant having cells which contain a transgene encoding a transgene expression product which desaturates a fatty acid molecule at carbon
10 5 from the carboxyl end of said fatty acid molecule, wherein said transgene is operably associated with an expression control sequence, under conditions whereby said transgene is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in said cells is altered.

15 20. A method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of:

growing a plant having cells which contain one or more transgenes, derived from a fungus or algae, which encodes a transgene expression product which desaturates a fatty acid molecule at a carbon selected from the group
20 consisting of carbon 5, carbon 6 and carbon 12 from the carboxyl end of said fatty acid molecule, wherein said one or more transgenes is operably associated with an expression control sequence, under conditions whereby said one or more transgenes is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in said cells is altered.

25

21. The method according to claims 19 or 20, wherein said long chain polyunsaturated fatty acid is selected from the group consisting of LA, ARA, GLA, DGLA, SDA and EPA.

22. A plant oil or fraction thereof produced according to the method of claims
19 or 20.
23. A method of treating or preventing malnutrition comprising administering
5 said plant oil of claim 22 to a patient in need of said treatment or prevention
in an amount sufficient to effect said treatment or prevention.
24. A pharmaceutical composition comprising said plant oil or fraction of claim
22 and a pharmaceutically acceptable carrier.
10
25. The pharmaceutical composition of claim 24, wherein said pharmaceutical
composition is in the form of a solid or a liquid.
26. The pharmaceutical composition of claim 25, wherein said pharmaceutical
15 composition is in a capsule or tablet form.
27. The pharmaceutical composition of claim 24 further comprising at least one
nutrient selected from the group consisting of a vitamin, a mineral, a
carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an
antioxidant, and a phenolic compound.
20
28. A nutritional formula comprising said plant oil or fraction thereof of claim
22.
29. The nutritional formula of claim 28, wherein said nutritional formula is
selected from the group consisting of an infant formula, a dietary
supplement, and a dietary substitute.
25

30. The nutritional formula of claim 29, wherein said infant formula, dietary supplement or dietary supplement is in the form of a liquid or a solid.

31. An infant formula comprising said plant oil or fraction thereof of claim 22.

5

32. The infant formula of claim 31 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

10

33. The infant formula of claim 32 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

15

34. A dietary supplement comprising said plant oil or fraction thereof of claim 22.

20

25

35. The dietary supplement of claim 34 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

36. The dietary supplement of claim 35 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium,

magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

37. The dietary supplement of claim 34 or claim 36, wherein said dietary supplement is administered to a human or an animal.
5
38. A dietary substitute comprising said plant oil or fraction thereof of claim 22.
39. The dietary substitute of claim 38 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.
10
40. The dietary substitute of claim 39 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.
15
41. The dietary substitute of claim 38 or claim 40, wherein said dietary substitute is administered to a human or animal.
20
42. A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patient said dietary substitute of claim 38 or said dietary supplement of claim 34 in an amount sufficient to effect said treatment.
25

43. The method of claim 42, wherein said dietary substitute or said dietary supplement is administered enterally or parenterally.

44. A cosmetic comprising said plant oil or fraction thereof of claim 22.

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45. The cosmetic of claim 44, wherein said cosmetic is applied topically.

46. The pharmaceutical composition of claim 24, wherein said pharmaceutical composition is administered to a human or an animal.

10

47. An animal feed comprising said plant oil or fraction thereof of claim 22.

15

48. An isolated nucleotide sequence comprising the nucleotide sequence selected from the group consisting of SEQ ID NO:38 - SEQ ID NO:44 wherein said nucleotide sequence is expressed in a plant cell.

49. The method of claim 20 wherein said fungus is *Mortierella species*.

50. The method of claim 49 wherein said fungus is *Mortierella alpina*.

20

51. An isolated nucleotide sequence selected from the group consisting of SEQ ID NO:49 - SEQ ID NO:50 wherein said sequence is expressed in a plant cell.

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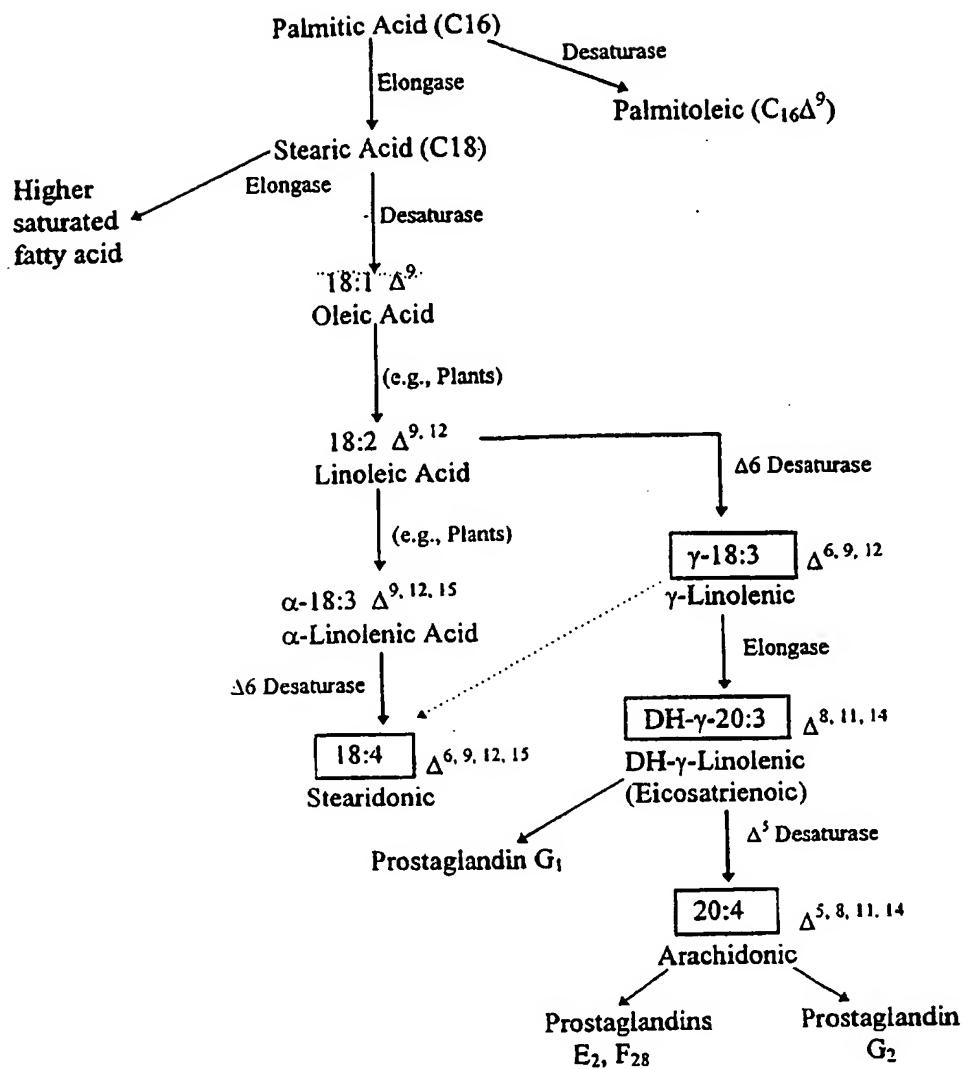


FIG. 1

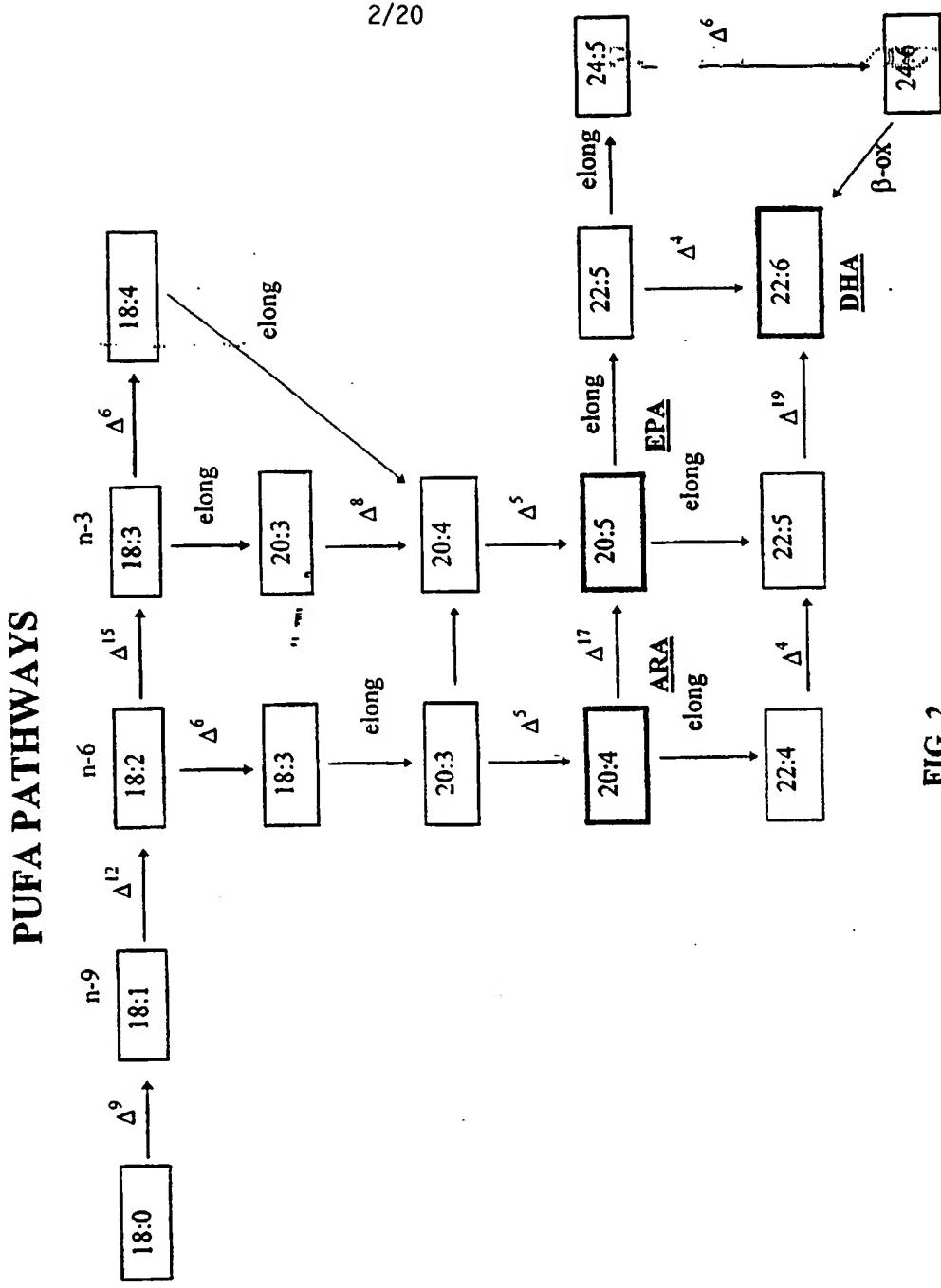


FIG. 2

60 *
CGACACTCCT TCCTTCTCT CACCCGTCCCT AGTCCCCCTTC AACCCCCCTTC TTTGACAAAG
ACAAACAAACC ATG GCT GCT CCC AGT GTG AGG ACG TTT ACT CGG GCC GAG
Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu

120 *
GTT TTG AAT GCC GAG GCT CTG AAT GAG GGC AAG AAG GAT GCC GAG GCA
Val Leu Asn Ala Glu Ala Leu Asn Glu Lys Lys Asp Ala Glu Ala

180 *
CCC TTC TTG ATG ATC ATC GAC AAC AAG GTG TAC GAT GTC GTC CGC GAG TTC
Pro Phe Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe

240 *
GTC CCT GAT CAT CCC GGT GGA AGT GTG ATT CTC ACG CAC GTT GGC AAG
Val Pro Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys

300 *
GAC GGC ACT GAC GTC TTT GAC ACT TTT CAC CCC GAG GCT GCT TGG GAG
Asp Gly Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu

360 *
ACT CTT GCC AAC TTT TAC GTT GGT GAT ATT GAC GAG AGC GAC CGC GAT
Thr Leu Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp

ATC AAG AAT GAT GAC TTT GCG GCC GAG GTC CGC AAG CTG CGT ACC TTG
Ile Lys Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu

FIG. 3A

TTC CAG TCT CTT GGT TAC TAC GAT TCT TCC AAG GCA TAC TAC GCC TTC Phe Gln Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe	420 *
AAG GTC TCG TTC AAC CTC TGC ATC TGG GGT TCG ACG GTC ATT GTC Lys Val Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val	480 *
GCC AAG TGG GGC CAG ACC TCG ACC CTC GCC AAC GTG CTC TCG CCT GCG Ala Lys Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala	540 *
CTT TRG GGT CTC TGC TGG CAG CAG TGC GGA TGG TRG GCT CAC GAC TRT Leu Leu Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe	600 *
TTG CAT CAC CAG GTC TTC CAG GAC CGT TTC TGG GGT GAT CTT TRC GGC Leu His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly	660 *
GCC TTC TTG GGA GGT GTC TGC CAG GGC TTC TCG TCC TCG TGG TGG AAG Ala Phe Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys	720 *
GAC AAG CAC AAC ACT CAC CAC GCC CCC AAC GTC CAC GGC GAG GAT Asp Lys His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp	780 *

FIG. 3B

CCC GAC ATT GAC ACC CAC CCT CTG TGG ACC TGG AGT GAG CAT GCG TGG
 Pro Asp Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu

 GAG ATG TTC TCG GAT GTC CCA GAT GAG GAG CTG ACC CGC ATG TGG TCG
 Glu Met Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser

 840 *

 CGT TTC ATG GTC CTC AAC CAG ACC TGG TTT TAC TTC CCC ATT CTC TCG
 Arg Phe Met Val Leu Asn Gln Thr Trp Phe Tyr Pro Ile Leu Ser

 900 *

 TTT GCC CGT CTC TCC TGG TGC CTC CAG TCC ATT CTC TTT GTG CCT
 Phe Ala Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro

 960 *

 AAC GGT CAG GCC CAC AAG CCC TCG GGC GCG CGT GTG CCC ATT TCG TGT
 Asn Gly Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu

 1020 *

 GTC GAG CAG CTG CTC GCG ATT CAC TGG ACC TGG TAC CTC GCC ACC
 Val Glu Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr

 1080 *

 ATG TTC CTG TTC ATC AAG GAT CCC GTC AAC ATT CTG GTG TAC TTT TGT
 Met Phe Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu

 GTC TCG CAG GCG GTG TGC GGA AAC TTG TTG GCG ATC GTG TAC TCG CTC
 Val Ser Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu

FIG. 3C

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1140	AAC CAC AAC GGT ATG CCT GTG ATC TCG AAG GAG GCG GTC GAT ATG Asn His Asn Gly Met Pro Val Ile Ser Lys Glu Ala Val Asp Met
1200	GAT TTC TTT ACG AAG CAG ATC ATC ACG GGT CGT GAT GTC CAC CCG GGT Asp Phe Phe Thr Lys Gln Ile Thr Gly Arg Asp Val His Pro Gly
1260	C [*] TA TTT GCC AAC TGG TTG ACG GGT GGA TTG AAC TAT CAG ATC GAG CAC Leu Phe Ala Asn Trp Phe Thr Gly Ile Asn Tyr Gln Ile Glu His
1320	CAC TTG TTT CCT TCG ATG CCT CGC CAC AAC TTT TCA AAG ATC CAG CCT His Leu Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro
1380	GCT GTC GAG ACC CTG TGC AAA AAG TAC AAT GTC CGA TAC CAC ACC ACC Ala Val Glu Thr Leu Cys Lys Tyr Asn Val Arg Tyr His Thr Thr
1440	GGT ATG ATC GAG GGA ACT GCA GAG GTC TTT AGC CGT CTG AAC GAG GTC Gly Met Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val
	TCC AAG GCT GCC TCC AAG ATG GGT AAG GCG CAG TAAAAAAA AAACAAAGGAC
	Ser Lys Ala Ala Ser Lys Met Gly Lys Ala Gln

FIG. 3D

1500 * GTTTTTTC GCAGTGCCT GTGCCGTGCT CGCTTCCCT TGTCAAGTCG AGCGTTCCTG
1560 * GAAAGGATCG TTCAAGTGAG TATCATCATT CTCCCTTAC CCCCCGCTCA TATCTCATTC
ATTTCCTTA TTAACAACT TGTTCCCCCC TTCACCG

FIG. 3E

HS24	[REDACTED]	LENNRATLLEIPEKLLVLSKLLAFLVSLMELNGISIVAKHGDISTLAKYLLGALLLGC	69
A115423	-	VILFATLAVAMSLGYLQVLACSVRNPONAGLLGC	38
12-5	-	CX	24
R42006	-	CX	3
M28140	-	C	0
R05219	-	C	0
HS3753	-	C	0
HS24	[REDACTED]	LENNRATLLEIPEKLLVLSKLLAFLVSLMELNGISIVAKHGDISTLAKYLLGALLLGC	119
A115423	[REDACTED]	SAYICBGSIVINSHSKWNA-[REDACTED]GATLSSGMDT[REDACTED]NARBLACHMSLDI	96
12-5	[REDACTED]	SAYICBGSIVINSHSKWNA-[REDACTED]GATLSSGMDT[REDACTED]NARBLACHMSLDI	83
R42006	-	SAYICBGSIVINSHSKWNA-[REDACTED]GATLSSGMDT[REDACTED]NARBLACHMSLDI	3
M28140	-	SAYICBGSIVINSHSKWNA-[REDACTED]GATLSSGMDT[REDACTED]NARBLACHMSLDI	0
R05219	-	SAYICBGSIVINSHSKWNA-[REDACTED]GATLSSGMDT[REDACTED]NARBLACHMSLDI	0
HS3753	-	SAYICBGSIVINSHSKWNA-[REDACTED]GATLSSGMDT[REDACTED]NARBLACHMSLDI	0
HS24	[REDACTED]	DEMUNNOOMEYEPILSEARISM	174
A115423	[REDACTED]	DEMUNNOOMEYEPILSEARISM	104
12-5	[REDACTED]	DEMUNNOOMEYEPILSEARISM	140
R42006	-	DEMUNNOOMEYEPILSEARISM	0
M28140	-	DEMUNNOOMEYEPILSEARISM	0
R05219	-	DEMUNNOOMEYEPILSEARISM	0
HS3753	-	DEMUNNOOMEYEPILSEARISM	0
HS24	[REDACTED]	INTTHIALATHLEJKOPVHLLV	229
A115423	F	INTTHIALATHLEJKOPVHLLV	104
12-5	F	INTTHIALATHLEJKOPVHLLV	185
R42006	-	INTTHIALATHLEJKOPVHLLV	29
M28140	-	INTTHIALATHLEJKOPVHLLV	33
R05219	-	INTTHIALATHLEJKOPVHLLV	1
HS3753	-	INTTHIALATHLEJKOPVHLLV	48
HS24	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	289
A115423	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	104
12-5	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	244
R42006	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	86
M28140	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	90
R05219	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	23
HS3753	[REDACTED]	PLVSOAIVCEHLLAIVESLNHHGMPVLSKRECAVDMOFEKOLIGADVHPGLEAHETGG	105
HS24	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	349
A115423	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	104
12-5	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	252
R42006	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	131
M28140	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	123
R05219	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	131
HS3753	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	143
HS24	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	355
A115423	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	104
12-5	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	252
R42006	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	131
M28140	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	123
R05219	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	131
HS3753	[REDACTED]	ENIQIEHLLFPESMCHHESKLLPVEFICKKHYHNYHTGMEGTAEVESRNLNEVSKAASI	143

FIG. 4

GTC CCG TGC GCA CAC CCG ATCC TCC CTC GCT C CGT CCT GGT TGT CCT TGC
 60 *
 CCACCGT GTC TCC CCA CCC TCG GAG AGGA CTG CAA CTG AAT CAG GAAC CGC CAA PAC
 120 *
 ACG ATT TCT TTT ACT CAGC ACC AACT CAA AAT CCT CAAC CGCA ACC CTT TTT CAGG ATG
 Met c
 GCA CCT CCC AAC ACT ATC GAT GCC GGT TTG ACC CAG CGT CAT ATC ACC
 Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile Ser
 180
 240 *
 AC C TCG GCG CCA AAC TCG CCC AAG CCT CCC TTC GAG CGC AAC TAC CAC
 Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr Gln
 300
 CTC CCC GAG TTC ACC ATC AAG GAG ATC CGA GAG TGC ATC CCT GCC CAC
 Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala His
 360 *
 TGC TTT GAG CGG TCC GGT CTC CGT CGT CCT TGC CAC GGT GCC ATC GGT
 Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile Asp
 420 *
 CTG ACT TCG GCG TCG CTC TCG TGC GCT GGT CCT GCG ACC CAG ATC GAC AG
 Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp Lys
 RTT GAG AAT CCC TCG ATC CGC TAT TCG GCC TGG CCT GTT TAC TGG ATC
 Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp Ile

FIG. 5A

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ATG CAG CGT ATT GTC TGC ACC GGT GTC TGG GTC CTC GCT CAC GAG TGT Met Glu Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu Cys	480
GGT CAT CAG TCC TCC TCG ACC ACC CTC AAC AAC ACA GTT GCT GGT Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val Gly	540
TGG ATC TGG CAC TCG ATG CTC TGG GTC CCC TAC CAC TCC TGG AGA ATC Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg Ile	600
TCG CAC TCG AAG CAC CAC AAG GCC ACT GGC CAT ATG ACC AAG GAC CAG Ser His Ser Lys His His Lys Ala Val Thr Gly His Met Thr Lys Asp Gln	660
GTC TTT GTC CCC AAG ACC CGC TCC CAG GTC GGC TGG CCT CCC AAG GAC Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys Glu	720
AAC GCT GCT GCT GCT GCT GCA GAG GAC ATG TCC GTG CAC CTG GAT Asn Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu Asp	780
GAG GAG GCT CCC ATT GTG ACT TTG TTG TGG ATG GTG ATC CAG TTC TGC Glu Glu Ala Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe Leu	840
	*
	*
	*
	*

FIG. 5B

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960 *

GCG CGC TGG ACC TCG CAC TTC CAC ACG TAC TCG CCC ATC TTT GAG CGC
Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu Pro

1020 *

CGC AAC TTT TTC GAC ATT ATC TCG GAC CTC GGT GTG TTG GCT GCC
Arg Asn Phe Phe Asp Ile Ile Ser Asp Leu Gly Val Leu Ala Ala

1080 *

CTC GGT GCC CTG ATC TAT GCC TCC ATG CAG TRG TCG CTC TRG ACC GTC
Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Thr Val

1140 *

TAC C AAG TAC TAT ATT GTC CCC TAC CTC TTT GTC AAC TTT TGG TTG GTC
Thr Lys Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu Val

1200 *

CTG ATC ACC TTC TTG CAG CAC ACC GAT CCC AAG CTG CCC CAT TAC CGC
Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr Arg

GAG GGT GCC TGG AAT TTC CAG CGT GGA GCT CTT TGC ACC GTT GAC CGC
Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp Arg

TCG TTT GGC AAG TTC TTG GAC CAT ATG TTC CAC GGC ATT GTC CAC ACC
Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His Thr

FIG. 5C

GAA GCT ACC TAT CAT CTC AAG AAA CTG CTC GGA GAG TAC TAT GTG TAC
 Glu Ala Thr Tyr His Leu Lys Leu Gly Glu Tyr Tyr Val Val Tyr
 1260
 GAC CCA TCC CCG ATC GTC GTC GCG GTC AGG TCC TTC CGT GAG TGC
 Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu Cys
 1320
 CGA TTC CTG GAC GAT CAG GGA GAC GTC GTC AAG AAG TAAAGA
 Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
 1380
 AAAAGACAAT GGACCCACACA CAACCTTGTC TCTACAGACC TAGTGTATCAT GTAGGCCATAC
 CACCTTCATAA AAGAACATGA GCTCTAGAGG CGCTGTATTC GCGCCCTCC
 1440

FIG. 5D

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FIG. 6

10 20 30 40 50 60 *

LHHTYTNIA G ADPDVSTSEP DVRRIKPNQK WFVNHNQHM FVPFLYGLLA FKVRIQDINI

70 80 90 100 110 120 *

LYFVKTNDAI RVNPISTWHT VMFWGGKAFF VVYRLIVPLQ YLPLGKVLL FTVADMVSSY

130 140 150 160 170 180 *

WLALTFQANY VVEEVQWPLP DENGIIQKD W AAMQVETTQD YAHDSHLWTS ITGSLNYQXV

HHLFPH

FIG. 7A

GCTCCCTCCA GTTCATGCCA CCTGCATTCT TTACGACCGT TAAGCAAG

60 * ATG GGA ACG GAC CAA GGA AAA ACC TTC ACC TGG GAA GAG CTG GCG GCG
Met Gly Thr Asp Gln Gly Lys Thr Phe Thr Trp Glu Glu Leu Ala Ala

120 * CAT AAC ACC AAG GAC GAC CTA CTC TTG GCC ATG CGC GGC AGG GTG TAC
His Asn Thr Lys Asp Asp Leu Leu Ala Ile Arg Gly Arg Val Tyr

180 * GAT GTC ACA AAG TTC TTG AGC CGC CAT CCT GGT GGA GTG GAC ACT CTC
Asp Val Thr Lys Phe Leu Ser Arg His Pro Gly Val Asp Thr Leu

240 * CTC CGA GCT GGC CGA GAT GTT ACT CCG GTC TTT GAG ATG TAT CAC
Leu Gly Ala Gly Arg Asp Val Thr Pro Val Phe Glu Met Tyr His

300 * GCG TTT GGG GCT GCA GAT ATT ATG AAG TAC TAT GTC CGT ACA
Ala Phe Gly Ala Ala Asp. Ala Ile Met Lys Tyr Tyr Val Gly Thr

360 * CTG GTC TCG AAT GAG CTG CCC ATC TTC CCG GAG CCA ACG GTG TTC CAC
Leu Val Ser Asn Glu Leu Pro Ile Phe Pro Glu Pro Thr Val Phe His

AAA ACC ATC AAG ACG AGA GTC GAG GGC TAC TTT ACG GAT CGG AAC ATT
Lys Thr Ile Lys Thr Arg Val Glu Gly Tyr Phe Thr Asp Arg Asn Ile

FIG. 7B

420 *

GAT CCC AAG AAT AGA CCA GAG ATC TGG GGA CGA TAC GCT GCT CRT ATC TTT
Asp Pro Lys Asn Arg Pro Glu Ile Trp Gly Arg Tyr Ala Leu Ile Phe

480 *

GGA TCC TTG ATC GCT TCC TAC GCG CAG CTC TTT GTG CCT TTC GTT
Gly Ser Leu Ile Ala Ser Tyr Tyr Ala Gln Leu Phe Val Phe Val

540 *

GTC GAA CGC ACA TGG CTT CAG GTG GTG TTT GCA ATC ATG GGA TTT
Val Glu Arg Thr Trp Leu Gln Val Val Phe Ala Ile Met Gly Phe

600 *

GCG TGC GCA CAA GTC GGA CTC AAC CCT CTT CAT GAT GCG TCT CAC TTT
Ala Cys Ala Gln Val Gly Leu Asn Pro Leu His Asp Ala Ser His Phe

660 *

TCA GTG ACC CAC AAC CCC ACT CTC TGG AAC ATT CTG GGA GCC ACC CAC
Ser Val Thr His Asn Pro Thr Val Trp Lys Ile Leu Gly Ala Thr His

720 *

GAC TTT TTC AAC GGA TCG TAC CTC GTG TGG ATG TAC CAA CAT ATG
Asp Phe Phe Asn Gly Ala Ser Tyr Leu Val Trp Met Tyr Glu His Met

CRC GGC CAT CAC CCC TAC ACC AAC ATT GCT GGA GCA GAT CCC GAC CTC
Leu Gly His His Pro Tyr Thr Asn Ile Ala Gly Ala Asp Pro Asp Val

FIG. 7C

TCG ACG TCT GAG CCC GAT GTT CGT CGT ATC AAG CCC AAC CAA AAG TGG
 Ser Thr Ser Glu Pro Asp Val Arg Arg Ile Lys Pro Asn Gln Lys Trp
 780

* TTT GTC AAC CAC ATC AAC CAG CAC ATG TTT GTT CCT TTC CTG TAC GGA
 Phe Val Asn His Ile Asn Gln His Met Phe Val Pro Phe Leu Tyr Gly
 840

CTC CTG GCG TTC AAG GTG CGC ATT CAG GAC ATC AAC ATT TTG TAC TTT.
 Leu Leu Ala Phe Lys Val Arg Ile Asn Asp Ile Asn Ile Leu Tyr Phe

900 *

GTC AAG ACC AAT GAC GCT ATT CGT GTC AAT CCC ATC TCG ACA TGG CAC
 Val Lys Thr Asn Asp Ala Ile Arg Val Asn Pro Ile Ser Thr Trp His

960 *

ACT GTG ATG RTC TGG GGC GGC AAG GCT RTC TTT GTC TGG TAT CGC CTC
 Thr Val Met Phe Trp Gly Gly Lys Ala Phe Phe Val Trp Tyr Arg Leu

1020

ATT GTT CCC CTG CAG TAT CTG CCC CTG GGC AAG GTG CTC CTC TTG TTC
 Ile Val Pro Leu Gln Tyr Leu Pro Leu Gly Lys Val Leu Leu Leu Phe

ACC GTC GCG GAC ATG CTG TCG TGT TAC TGG CTG GCG CTG ACC TTC CAG
 Thr Val Ala Asp Met Val Ser Ser Tyr Trp Leu Ala Leu Thr Phe Gln

FIG. 7D

1080 GCG AAC CAC GAT GTT GAG GAA GTT CAG TGG CCG TTG CCT GAC GAG AAC
 Ala Asn His Val Val Glu Glu Val Glu Val Trp Pro Leu Pro Asp Glu Asn

 1140 GCG ATC ATC CAA AAG GAC TGG GCA GCT ATG CAG GTC GAG ACT ACG CAG
 Gly Ile Ile Gln Lys Asp Trp Ala Ala Met Gln Val Glu Thr Thr Gln

 1200 GAT TAC GCA CAC GAT TCG CAC CTC TGG ACC AGC ATC ACT GGC AGC TTG.
 Asp Tyr Ala His Asp Ser His Leu Trp Thr Ser Ile Thr Gly Ser Leu

 1260 AAC TAC CAG CAC GCT GTG CAC CAT CTG CTC CCO AAC GTC TCG CAG CAC CAT
 Asn Tyr Gln Ala Val His His Leu Phe Pro Asn Val Ser Gln His His His

 1320 TAT CCC GAT ATT CTG GCC ATC ATC AAG AAC ACC TGC AGC GAG TAC AAG
 Tyr Pro Asp Ile Leu Ala Ile Ile Lys Asn Thr Cys Ser Glu Tyr Lys

 1380 GTT CCA TAC CTT GTC AAG GAT ACG TTT TGG CAA GCA TTT GCT TCA CAT
 Val Pro Tyr Leu Val Lys Asp Thr Phe Trp Gln Ala Phe Ala Ser His

 1440 TTT GAG CAC TTG CGT GTT CTT GGA CTC CGT CCC AAG GAA GAG TAGA
 Leu Glu His Leu Arg Val Leu Gly Leu Arg Pro Lys Glu Glu

 1500 CTAAGTGACAG TTCTCTATGCA AGA

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FIG. 8

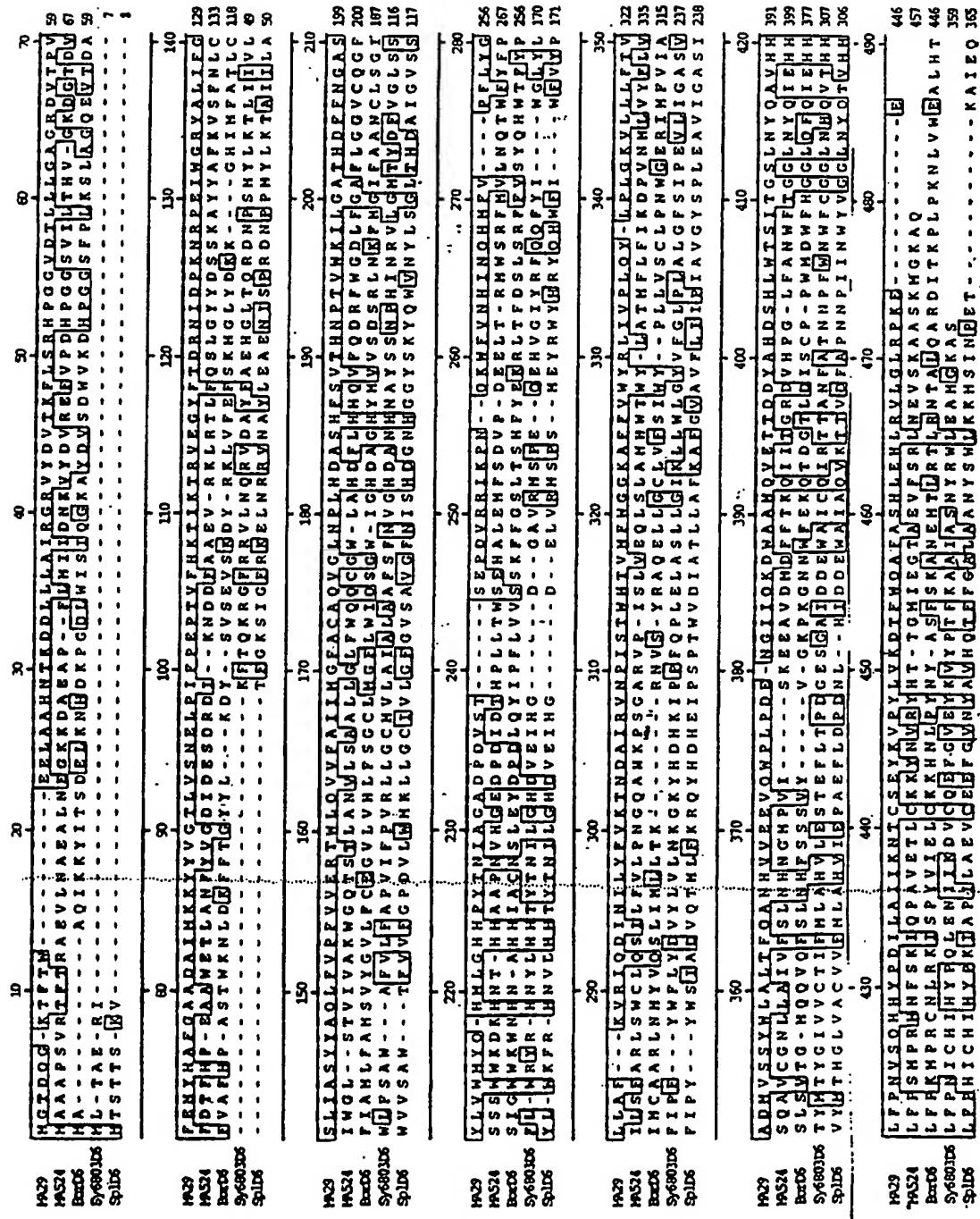


FIG. 8

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FastA Match of ma29 and contig 253538a

SCORES Init1: 117 Initn: 225 Opt: 256
 Smith-Waterman score: 408; 27.0% identity in 441 aa overlap

	10	20	30	40	50	
ma29gcf.pep	MGTDQGKT---FTWEELAAHNTKDDLLLAI	RGRVYDVTKF	LSRHPGGVDT	LLL	GAGR	
253538a	QGPTPRYFTWDEVAQRSGCEERWLVIDRKVN	I	SEFTRRRH	P	PGGSRVISHYAGQDAT	
	10	20	30	40	50	
ma29gcf.pep	60	70	80	90	100	110
253538a	PVFEMYHAF-GAADAIMKKYYVGTLVSNELPI	FPEPTVFHK	TVEGYFTDRN	IDPKN		
	DPFVAFHINKGLVKKYMNSLLIGEL-SPEQPSF-	EPTK	NKELT	DEFRE	LRA	TMGLMK
	60	70	80	90	100	110
ma29gcf.pep	120	130	140	150	160	170
253538a	RPEIWGRYALIFGSLIASYYAQLF	VPFVV	ERTWLQ	VVF-AIIMGFAC	AQVGLNPLHDASH	
	ANHVF--FLLYL	HILLLDGA	AWTLWVFGTSFL	FLLCAVLLSAVQAQAGWLQ-HDYGH		
	120	130	140	150	160	170
ma29gcf.pep	180	190	200	210	220	
253538a	FSVTHNPTVW	KILGATHDF	---	FNGASYL	VWMYQHMLGH	HPYTNIA
	GSY	Y		MLGHH	PYTNIA	AGADPDVSTSE
	LSVYRKPK-WNHL	--VHKFVIGH	LKGASANWWNHRH	-FQHHAKPNIFHKD	PDVNMLHV	FV
	180	190	200	210	220	
ma29gcf.pep	230	240	250	260	270	280
253538a	---	PDVRRIKP	NQKWF-VNHINQHM	FLYGLLA	FKVRIQDINILYFVK	TNDAIRV
		FNQKWF	HM	FLYGLLA	FKVRIQDINILYFVK	TNDAIRV
	LGEWQPIEY	GKKKL	KYL	LPYNHQHEYFFLIGP	PLLIPMYFQYQI	IMTMIVHKNWVDL
	230	240	250	260	270	280
ma29gcf.pep	290	300	310	320	330	340
253538a	NPISTWHTVMFWGGKAFFVWYRLIVPLQY	YRPLGLKV	LLLFTVADMVSSYWLALT	TFQANHVV		
	YRPLGLKV	LLLFTVADMVSSYWLALT	TFQANHVV			
	-----AWAVSYYI	---	RFFITY	IPF-YGILG-ALLFLNFIR	FLESHW	FVWVTQMNHIV
	290	300	310	320	330	340
ma29gcf.pep	350	360	370	380	390	
253538a	EEVQWPLPDENGIIQKDWAAMQVETT	---	QDYAHDSHLWTSITG	SLYQAVHHLFPNV		
	EEVQWPLPDENGIIQKDWAAMQVETT	---	QDYAHDSHLWTSITG	SLYQAVHHLFPNV		
	MEI-----DQEAY	--RDWFSSQLTATCNVEQSFFND	---	WFS--GHLNFQIEHHLFPTMP		
	340	350	360	370	380	
ma29gcf.pep	400	410	420	430	440	
253538a	QHHYPDILAIKNTCSEYKPVYLV	KDTFWQAFASH	LEHRLVLRPKEEX			
	RHN	LHKIA	PLVKS	CAKHGIEYQE	KPLRALLDI	IRSLKKSGKLWDAYLHKX
	380	390	400	410	420	430

Figure 9

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FastA Match of ma524 and contig 253538a

SCORES Init1: 231 Initn: 499 Opt: 401
 Smith-Waterman score: 620; 27.3% identity in 455 aa overlap

	10	20	30	40	50	59
ma524gcf.pep	MAAAPSVRTFTRAEVLNAAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGSVILTH-:: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	QGPTPRYFIWDEV-----AQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHY: : :: : :: : :: : :: : :: : :: : :: : :: :				
	10	20	30	40	50	59
	60	70	80	90	100	110
ma524gcf.pep	VGKDGTDFVFDIFHPEAAW--ETLANFYVGDIDE---SDRDIKNDDFAAEVRKLRITLFQSL: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	AGQDATDPFVAFHINKGLVKKYMNSLLIGELSPEQPSFEPTKNELTDEFRELATVERM: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
	60	70	80	90	100	110
	120	130	140	150	160	170
ma524gcf.pep	GYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHD: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	GLMKANHVFFLLYLLHILLLDGAALWTLWVFG-TSFLPFLLCAVILSAVQAQAGWLQHDY: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
	120	130	140	150	160	170
	180	190	200	210	220	230
ma524gcf.pep	LHHQVFQDRFWGDLFGAFLGGVCQGFSSSWKDKHNTHHAAPNVHGEDPDIDTHPLLTWS: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	GHLSVYRKPKWNHLVHKFVIGHLKKGASANWWNHRFQHHAKPNIFHKDPPVN---ML---: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
	170	180	190	200	210	220
	240	250	260	270	280	290
ma524gcf.pep	EHALEMFSDVPEELTRMWSRFMVNLNQWTWFYFPILS---FARLSWCLOSILFVLPNCQAH: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	-HVF-VLGEWQPIEYGKKKLKYLPYNHQHEYFFLIGPPLLIPMYFQYQIIMIMI---VH: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
	230	240	250	260	270	280
	300	310	320	330	340	349
ma524gcf.pep	KPSGARVPISLVEQLSLAMHWTWYLATMFLFIK--DPVNMLVYFLVSQAVCGNLLAIVFS: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	K-----NWVDLAWAVSYIIRFFITYIPFYGILGALLFLNFIRFLESHWFVWVTQ: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
	280	290	300	310	320	349
	350	360	370	380	390	400
ma524gcf.pep	LNHNGMPVISKEEAVDMDFITKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNF: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	MNHIVMEI--DQEAYR-DWFSQLTATCNVEQSFFNDWFSGHLMFQIEHHLFPTMPRHNL: : :: : :: : :: : :: : :: : :: : :: : :: : :: :				
	330	340	350	360	370	380
	410	420	430	440	450	
ma524gcf.pep	SKIQPAVETLCCKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQX: : :: : :: : :: : :: : :: : :: : :: : :: :				
253538a	HKIAPLVKSLCAKHGIEYQEKPILLRALLDIIRSLKKSGLWLDAYLHKX: : :: : :: : :: : :: : :: : :: : :: : :: :				
	390	400	410	420	430	

Figure 10

INTERNATIONAL SEARCH REPORT

International Application No PCT/US 98/07421

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6	C12N15/53	C12N15/82	C12N5/10	C12P7/64	C11B1/00
	A61K31/20	A23L1/30	A23K1/00		

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C12P C11B A61K A23L A23K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 93 06712 A (RHONE POULENC AGROCHIMIE) 15 April 1993 cited in the application see the whole document ---	20-22
X	WO 94 18337 A (MONSANTO CO ;UNIV MICHIGAN (US); GIBSON SUSAN IRMA (US); KISHORE G) 18 August 1994 * see the whole document, esp. claims 8-10 * ---	20-47
X	WO 96 21022 A (RHONE POULENC AGROCHIMIE) 11 July 1996 cited in the application * see the whole document, esp. p. 2 1.3-21 * ---	20-47
	-/-	

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the International filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

Date of mailing of the International search report

21 August 1998

03/09/1998

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Kania, T

INTERNATIONAL SEARCH REPORT

In	nternational Application No
PCT/US 98/07421	

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0 561 569 A (LUBRIZOL CORP) 22 September 1993 cited in the application see the whole document ----	20-47
A	COVELLO P. ET AL.: "Functional expression of the extraplastidial Arabidopsis thaliana oleate desaturase gene (FAD2) in Saccharomyces cerevisiae" PLANT PHYSIOLOGY, vol. 111, no. 1, May 1996, pages 223-226, XP002075211 see the whole document ----	1-51
A	WO 94 11516 A (DU PONT ;LIGHTNER JONATHAN EDWARD (US); OKULEY JOHN JOSEPH (US)) 26 May 1994 cited in the application see the whole document ----	1-51
T	WO 97 30582 A (CARNEGIE INST OF WASHINGTON ;MONSANTO COMPANY INC (US); BROUN PIER) 28 August 1997 see the whole document -----	1-51

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/07421

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 23, 42, 43 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/ US 98/07421

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (group of) inventions in this international application, as follows:

1. Claims 1-47, 49,50

Nucleic acid constructs comprising delta-5, delta-6, or delta-12 desaturases according to SEQ ID NO: 1,3,5, derived from the fungus *Mortierella alpina*. Recombinant plant cells comprising said constructs.

Methods for obtaining altered long chain polyunsaturated fatty acid biosynthesis using plants comprising delta-5, delta-6, or delta-12 desaturases, or combinations thereof, derived from fungi or algae.

Plant oils derived from said plants and their use for therapeutical, nutritional, and cosmetical purposes, as well as products derived therefrom.

2. Claim : 48

An isolated sequence comprising the nucleotide sequence selected from the group of SEQ ID NO: 38-44, wherein said nucleotide is expressed in a plant cells.

3. Claim : 51

An isolated nucleotide sequence selected from the group consisting of SEQ ID NO: 49-50, wherein said sequence is expressed in a plant cell.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/07421

Patent document cited in search report	Publication date	Patent family member(s)			Publication date
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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/07421

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9730582 A	28-08-1997	AU 2050497 A	10-09-1997